



Your request has been successfully submitted and put into the Blast Queue.

Query = (1708 letters)

SEQ ID NO: 5
(nr)

The request ID is 1060818008-0485-22286

Format! or **Reset all**

The results are estimated to be ready in 33 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi Alignment in HTML

Number of: Descriptions 100 Alignments 50

Alignment view Hit Table

Start formatting
from query #

Limit results by
entrez query or select from: (none)

Expect value
range:

Results file ☐



Your request has been successfully submitted and put into the Blast Queue.

Query = (3412 letters)

SEQ ID NO: 6
(NR)

The request ID is 1060818067-0938-25515

Format! or **Reset all**

The results are estimated to be ready in 28 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi Alignment in

Number of: Descriptions Alignments

Alignment view

Start formatting from query #

Limit results by or select from:

Expect value range:

Results file ☐

 **NCBI**
Nucleotide Protein Translations Retrieve results for an RID

formatting **BLAST**

Your request has been successfully submitted and put into the Blast Queue.

Query = (1946 letters)

SEQ ID NO: 7
(7R)

The request ID is 1060818116-8188-1510948.BLASTQ4

Format! or **Reset all**

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi Alignment ▼ in HTML

Number of: Descriptions 100 ▼ Alignments 50 ▼

Alignment view Hit Table ▼

Start formatting
from query #

Limit results by or select from: (none) ▼
entrez query

Expect value
range:

Results file ☐

**formatting BLAST**

Nucleotide

Protein

Translations

Retrieve results for an RID

Your request has been successfully submitted and put into the Blast Queue.

Query = (3283 letters)

SEQ ID NO:8
(nr)

The request ID is 1060818177-8586-2227958.BLASTQ4

Format! or **Reset all**

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi Alignment in

Number of: Descriptions Alignments

Alignment view

Start formatting
from query #

Limit results by
entrez query or select from:

Expect value
range:

Results file ☐



results of BLAST

TBLASTX 2.2.6 [Apr-09-2003]

RID: 1061911388-17096-1581453.BLASTQ3

Query=

(1708 letters)

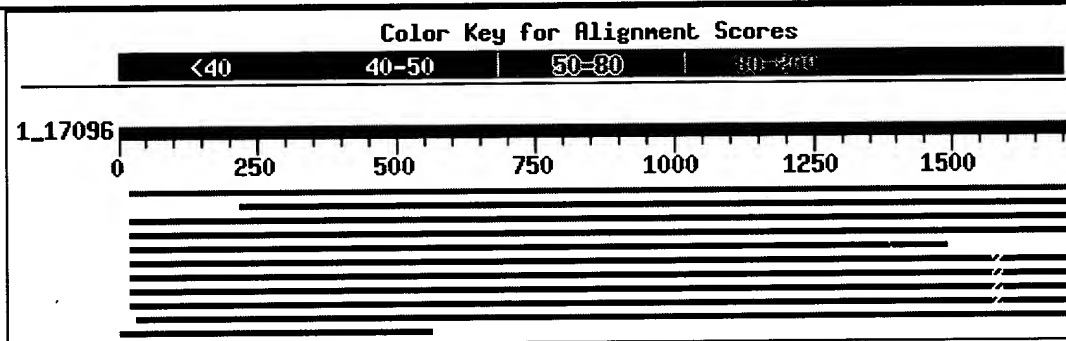
*translated
seq 5*

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)
1,886,208 sequences; 8,918,056,233 total letters

Taxonomy reports

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score E
(bits) Value N

gi 4191607 gb AF117106.1 AF117106	Homo sapiens IGF-II m...	709	0.0	6	LUG
gi 21361351 ref NM_006546.2	Homo sapiens IGF-II mRNA-b...	576	0.0	6	LUG
gi 7141071 gb AF198254.1 AF198254	Homo sapiens mRNA-bin...	576	0.0	6	LUG
gi 24580458 gb AC105030.11	Homo sapiens chromosome 17,...	363	0.0	12	
gi 22760672 dbj AK074915.1	Homo sapiens cDNA FLJ90434 ...	709	0.0	4	UG
gi 3273748 gb AF061569.1 AF061569	Mus musculus coding r...	525	0.0	9	LUG
gi 31560605 ref NM_009951.2	Mus musculus insulin-like ...	525	0.0	9	LG
gi 12851513 dbj AK013940.1	Mus musculus 13 days embryo...	525	0.0	9	LUG
gi 26336870 dbj AK044850.1	Mus musculus 9.5 days embryo...	525	0.0	9	LU
gi 30354043 gb BC051679.1	Mus musculus insulin-like gr...	522	0.0	9	L
gi 31342209 ref NM_175594.2	Rattus norvegicus IGF-II m...	529	0.0	7	L
gi 27464837 gb AF541940.1	Rattus norvegicus b-actin zi...	529	0.0	7	L
gi 2570920 gb AF026527.1 AF026527	Gallus gallus zipcode...	504	0.0	6	
gi 27689046 ref XM_220886.1	Rattus norvegicus similar ...	529	0.0	6	L
gi 22204252 emb AL606704.20	Mouse DNA sequence from cl...	218	0.0	15	
gi 21954991 gb AC098642.5	Genomic sequence for Mus mus...	218	0.0	14	

gi 14475918 gb AC084407.10	Mus Musculus Strain C57BL6/...	218	0.0	14	
gi 3172448 gb AF064634.1 AF064634	Xenopus laevis Vg1 RN...	341	0.0	5	
gi 3136157 gb AF055923.1 AF055923	Xenopus laevis RNA bi...	341	0.0	5	
gi 2801765 gb AF042353.1 AF042353	Xenopus laevis KH dom...	341	0.0	5	
gi 3172446 gb AF064633.1 AF064633	Xenopus laevis Vg1 RN...	341	0.0	5	
gi 28278435 gb BC045873.1	Danio rerio decapentaplegic ...	336	0.0	5	L
gi 18858570 ref NM 131491.1	Danio rerio decapentaplegi...	336	0.0	5	L
gi 5596631 gb AF161270.1 AF161270	Danio rerio Vg1 RNA b...	336	0.0	5	L
gi 30795211 ref NM 006547.2	Homo sapiens IGF-II mRNA-b...	374	0.0	5	L G
gi 4191611 gb AF117108.1 AF117108	Homo sapiens IGF-II m...	374	0.0	5	L G
gi 29145080 gb BC049082.1	Mus musculus insulin-like gr...	377	0.0	5	L
gi 12847972 dbj AK011689.1	Mus musculus 10 days embryo...	377	0.0	5	L G
gi 28175448 gb BC045138.1	Mus musculus insulin-like gr...	377	0.0	5	L
gi 11933383 dbj AB046173.1	Mus musculus mimp3 mRNA for...	377	0.0	5	L G
gi 2105468 gb U97188.1 HSU97188	Homo sapiens putative R...	374	0.0	5	L G
gi 4098296 gb U76705.1 HSU76705	Human putative RNA bind...	374	0.0	5	L G
gi 31542991 ref NM 023670.2	Mus musculus insulin-like ...	377	0.0	5	L G
gi 26353479 dbj AK088465.1	Mus musculus 2 days neonate...	377	0.0	5	L
gi 27552765 ref NM 006548.2	Homo sapiens IGF-II mRNA-b...	327	0.0	5	L
gi 33878041 gb BC021290.2	Homo sapiens IGF-II mRNA-bin...	327	0.0	5	L
gi 4191609 gb AF117107.1 AF117107	Homo sapiens IGF-II m...	327	0.0	5	L
gi 26093366 dbj AK049196.1	Mus musculus ES cells cDNA,...	324	0.0	6	L
gi 23958572 gb BC023758.1	Mus musculus RIKEN cDNA C330...	324	0.0	6	L
gi 26090647 dbj AK044984.1	Mus musculus 9.5 days embryo...	324	0.0	6	L
gi 4883680 gb AF057352.1 AF057352	Homo sapiens hepatoce...	327	0.0	4	
gi 26097330 dbj AK077404.1	Mus musculus 6 days neonate...	324	e-179	7	L
gi 27666189 ref XM 221343.1	Rattus norvegicus similar ...	315	e-175	5	L
gi 33942111 ref NM 183029.1	Mus musculus RIKEN cDNA C3...	313	e-173	5	L
gi 32451876 gb BC054552.1	Mus musculus cDNA clone MGC:...	313	e-173	5	L
gi 7656675 gb AC020629.6	Homo sapiens 12q BAC RP11-76E...	235	e-161	6	
gi 3646096 emb AL023775.1 HS497J21	Human DNA sequence f...	308	e-152	6	
gi 15552942 emb AL596177.4	Human DNA sequence from clo...	285	e-142	5	
gi 19849375 gb AC104980.5	Homo sapiens chromosome 8, c...	259	e-133	5	
gi 17298202 dbj AP004290.2	Homo sapiens genomic DNA, c...	259	e-133	5	
gi 27413166 gb AC016961.28	Homo sapiens 3 BAC RP11-394...	100	e-126	10	
gi 33284913 emb BX088533.9	Zebrafish DNA sequence from...	95	e-120	9	
gi 26081662 dbj AK030096.1	Mus musculus adult male tes...	205	e-111	4	
gi 27710325 ref XM 231739.1	Rattus norvegicus similar ...	376	e-101	2	L
gi 30148117 ref XM 291469.2	Homo sapiens similar to he...	264	3e-94	3	L
gi 18873962 gb AC092447.5	Homo sapiens BAC clone RP11-...	250	3e-89	4	L
gi 30520355 ref NG 002770.1	Homo sapiens pseudogene of...	250	3e-89	4	L
gi 30151067 ref XM 302320.1	Homo sapiens similar to IG...	242	4e-87	4	L
gi 31240026 ref XM 320427.1	Anopheles gambiae ENSANGP0...	122	4e-86	5	
gi 28492961 ref XM 193835.2	Mus musculus RIKEN cDNA C3...	323	1e-85	3	L
gi 21637524 gb AC091133.11	Homo sapiens chromosome 17,...	232	3e-85	5	
gi 28571360 ref NM 167254.2	Drosophila melanogaster IG...	124	3e-84	5	L
gi 17862977 gb AY069821.1	Drosophila melanogaster SD07...	124	3e-84	5	L
gi 7533028 gb AF241237.1 AF241237	Drosophila melanogast...	124	4e-84	5	L
gi 24641109 ref NM 167255.1	Drosophila melanogaster IG...	124	5e-84	5	
gi 28571361 ref NM 078556.3	Drosophila melanogaster IG...	124	5e-84	5	

gi 24641096 ref NM_167249.1	Drosophila melanogaster IG...	124	6e-84	5
gi 24641098 ref NM_167250.1	Drosophila melanogaster IG...	124	7e-84	5
gi 24641104 ref NM_167253.1	Drosophila melanogaster IG...	124	9e-84	5
gi 24641102 ref NM_167252.1	Drosophila melanogaster IG...	124	9e-84	5
gi 24641100 ref NM_167251.1	Drosophila melanogaster IG...	124	9e-84	5
gi 25012806 gb BT001739.1	Drosophila melanogaster RE72...	124	2e-83	5
gi 30581644 gb AC094527.7	Rattus norvegicus 5 BAC CH23...	122	3e-80	9
gi 13446341 gb AC021876.5	Homo sapiens BAC clone GS1-1...	121	9e-80	5
gi 27485839 ref XM_208686.1	Homo sapiens similar to he...	192	8e-77	3
gi 532210 gb L35549.1 MUSYBIC	Mus musculus Y-box bindin...	169	2e-72	5
gi 13446351 gb AC005082.3	Homo sapiens BAC clone CTA-2...	94	2e-54	5
gi 27710263 ref XM_216143.1	Rattus norvegicus similar ...	205	4e-50	2
gi 25100579 gb AC125292.4	Drosophila melanogaster X BA...	125	3e-39	4
gi 22832049 gb AE003484.2	Drosophila melanogaster chro...	125	9e-38	4
gi 28514171 ref XM_286404.1	Mus musculus hypothetical ...	74	4e-31	5
gi 26102680 dbj AK085396.1	Mus musculus 0 day neonate ...	69	1e-29	5
gi 33086575 gb AY325199.1	Rattus norvegicus Ab2-255 mR...	119	7e-27	2
gi 26090795 dbj AK045244.1	Mus musculus 9.5 days embry...	124	8e-26	1
gi 27709099 ref XM_228991.1	Rattus norvegicus similar ...	100	2e-18	1
gi 17554287 ref NM_065522.1	Caenorhabditis elegans put...	51	5e-15	3
gi 508101 emb Z34802.1 CEM88	Caenorhabditis elegans cos...	51	2e-12	3
gi 32423212 ref XM_332043.1	Neurospora crassa strain O...	56	7e-12	2
gi 26330215 dbj AK034811.1	Mus musculus 12 days embryo...	51	6e-11	4
gi 10947013 ref NM_021568.1	Mus musculus poly(rC) bind...	51	6e-11	4
gi 9957160 gb AF176327.1 AF176327	Mus musculus alphaCP-...	51	6e-11	4
gi 27503478 gb BC042440.1	Mus musculus poly(rC) bindin...	51	6e-11	4
gi 2644965 emb AJ003023.1 OCHNRNPE1	Oryctolagus cunicul...	49	1e-10	4
gi 14141164 ref NM_006196.2	Homo sapiens poly(rC) bind...	49	2e-10	4
gi 24980782 gb BC039742.1	Homo sapiens, clone MGC:4756...	49	2e-10	4
gi 444020 emb Z29505.1 HSNUACBIP	H.sapiens mRNA for nuc...	49	2e-10	4
gi 460770 emb X78137.1 HSRNPE1	H.sapiens hnRNP-E1 mRNA	49	2e-10	4
gi 1215670 gb U24223.1 HSU24223	Human alpha-CP1 mRNA, c...	49	2e-10	4
gi 26348075 dbj AK079564.1	Mus musculus adult male hyp...	51	3e-10	3
gi 21753334 dbj AK094301.1	Homo sapiens cDNA FLJ36982 ...	51	3e-10	3

Alignments

>gi|4191607|gb|AF117106.1|AF117106 Homo sapiens IGF-II mRNA-binding protein
Length = 2130

Score = 709 bits (1543), Expect(4) = 0.0
Identities = 306/335 (91%), Positives = 308/335 (91%)
Frame = +2 / +1

Query: 704 AMSSHLIPGLNLAAGVGLFXXXXXXXXXXXXXXXXXTGAAPYSSFMQAPEQEMVQVFIPAQAVG 883
++ SHLIPGLNLAAGVGLF TGAAPYSSFMQAPEQEMVQVFIPAQAVG
Sbjct: 1084 SLQSHLIPGLNLAAGVGLFPASSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVG 1263

Query: 884 AIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGLKEEN 1063
AIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGLKEEN
Sbjct: 1264 AIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGLKEEN 1443

Query: 1064 FFGPKKEEVKLETHIRVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVK 1243
 FFGPKKEEVKLETHIRVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVK
 Sbjct: 1444 FFGPKKEEVKLETHIRVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVK 1623

Query: 1244 IIGHFYASQMAQRKIRDILAQVKQQHQKGQSNQAQARRKXXXXXXXXXXESRTTGRNRECA 1423
 IIGHFYASQMAQRKIRDILAQVKQQHQKGQSNQAQARRK ESRTTGRNRECA
 Sbjct: 1624 IIGHFYASQMAQRKIRDILAQVKQQHQKGQSNQAQARRK*PAPPCPFESRTTGRNRECA 1803

Query: 1424 LPGRPENEWESGTGPGCRSGLPT*LRKMFQ*GTILIXQPQTPTQLAQHCXPLGVSEIXAQ 1603
 LPGRPENEWESGT GPGCRSGLPT*LRKMFQ*GTIL QPQTPTQLAQHC PLGVSEI AQ
 Sbjct: 1804 LPGRPENEWESGTPGPGCRSGLPT*LRKMFQ*GTILISQPQTPTQLAQHCLPLGVSEILAQ 1983

Query: 1604 GTFKRGLFKEALQAPPRGWITPWEEK*NFLQVLK 1708
 GTFKRGLFKEALQAPPRGWITPWEEK*NFLQVLK
 Sbjct: 1984 GTFKRGLFKEALQAPPRGWITPWEEK*NFLQVLK 2088

Score = 644 bits (1400), Expect(5) = 0.0
 Identities = 265/290 (91%), Positives = 265/290 (91%)
 Frame = +3 / +2

Query: 837 PSRRWCRCCLSPPRQWAPXXXXXXXXXXXXXGLPAPPSRLHHPKHLTPKFVWLSSLDRQRP 1016
 PSRRWCRCCLSPPRQWAP PGLPAPPSRLHHPKHLTPKFVWLSSLDRQRP
 Sbjct: 1217 PSRRWCRCCLSPPRQWAPSSARRGSTSNSSPGLPAPPSRLHHPKHLTPKFVWLSSLDRQRP 1396

Query: 1017 NSRLREESMANSRRRTSLVPRRK*SWRPTYVCQHQQLAGSLAKVEKR*TSCRI*RQLRW* 1196
 NSRLREESMANSRRRTSLVPRRK*SWRPTYVCQHQQLAGSLAKVEKR*TSCRI*RQLRW*
 Sbjct: 1397 NSRLREESMANSRRRTSLVPRRK*SWRPTYVCQHQQLAGSLAKVEKR*TSCRI*RQLRW* 1576

Query: 1197 YQETRPLMRTTRSS*KSSDISMPVRWLNGRSETSWPRLSSSIRRDRVTRPRHGGSDQPLP 1376
 YQETRPLMRTTRSS*KSSDISMPVRWLNGRSETSWPRLSSSIRRDRVTRPRHGGSDQPLP
 Sbjct: 1577 YQETRPLMRTTRSS*KSSDISMPVRWLNGRSETSWPRLSSSIRRDRVTRPRHGGSDQPLP 1756

Query: 1377 VPXSPGQQRAEIESVLSPAGLRMSGNPGHXGRAVDQVCPLD*ERCXXXXXXXXXXKHPPN 1556
 VP SPGQQRAEIESVLSPAGLRMSGNPGH GRAVDQVCPLD*ERC KHPPN
 Sbjct: 1757 VPSSPGQQRAEIESVLSPAGLRMSGNPGHLGRAVDQVCPLD*ERCSEEP*SLSPKHPPN 1936

Query: 1557 WPNTVCPSGCQKX*RKALLNVDCLKKLSRPHQEGGSHLSGKKNKISFRF* 1706
 WPNTVCPSGCQK *RKALLNVDCLKKLSRPHQEGGSHLSGKKNKISFRF*
 Sbjct: 1937 WPNTVCPSGCQKF*RKALLNVDCLKKLSRPHQEGGSHLSGKKNKISFRF* 2086

Score = 634 bits (1378), Expect(4) = 0.0
 Identities = 267/283 (94%), Positives = 267/283 (94%)
 Frame = -3 / -3

Query: 1706 LKPEGNFIFLPTEV*STLLVGPGEELL*TIHV*KCLALXFLTPRGAXSVGPIGWVFGAXRS 1527
 LKPEGNFIFLPTEV*STLLVGPGEELL*TIHV*KCLAL FLTPRGA SVGPIGWVFGA RS
 Sbjct: 2086 LKPEGNFIFLPTEV*STLLVGPGEELL*TIHV*KCLALEFLTPRGADSVGPIGWVFGAERS 1907

Query: 1526 GFLTGTFSFSIKWANLIYSPAQVSRIPTHSQACRGEHTLDFCPLLSWTXRDREGLVTXXXX 1347
 GFLTGTFSFSIKWANLIYSPA VSRIPTHSQACRGEHTLDFCPLLSWT RDREGLVT
 Sbjct: 1906 GFLTGTFSFSIKWANLIYSPAQVSRIPTHSQACRGEHTLDFCPLLSWTRRDREGLVTSSVP 1727

Query: 1346 XXXXXXSDAAA*PGPGCLGSSVEPSDWHNR*FSR*PGRSHQGSGLLVLPQLPSNSA 1167
SDAAA*PGPGCLGSSVEPSDWHNR*FSR*PGRSHQGSGLLVLPQLPSNSA
Sbjct: 1726 GPGYSVPSDAAA*PGPGCLGSSVEPSDWHNR*FSR*PGRSHQGSGLLVLPQLPSNSA 1547

Query: 1166 TRSPFFHLCQ*PGQLMLAHVCGSPASLPPWDQRSSPP*VCHRRFFPEP*IGPLAVQ***P 987
TRSPFFHLCQ*PGQLMLAHVCGSPASLPPWDQRSSPP*VCHRRFFPEP*IGPLAVQ***P
Sbjct: 1546 TRSPFFHLCQ*PGQLMLAHVCGSPASLPPWDQRSSPP*VCHRRFFPEP*IGPLAVQ***P 1367

Query: 986 YELWSQVFRVVQS*WRRWQTGRAV*CAAPSCR*WRPLPGRG*T 858
YELWSQVFRVVQS*WRRWQTGRAV*CAAPSCR*WRPLPGRG*T
Sbjct: 1366 YELWSQVFRVVQS*WRRWQTGRAV*CAAPSCR*WRPLPGRG*T 1238

Score = 557 bits (1211), Expect(3) = 0.0
Identities = 228/237 (96%), Positives = 233/237 (98%)
Frame = -1 / -1

Query: 739 QVQARDQVRAHGSIIILIGLPNFLHYFLLGPATILDGPLHSDGPLRVVKGKVLQRGDGDF 560
Q + + +++AHGSIIILIGLPNFLHYFLLGPATILDGPLHSDGPLRVVKGKVLQRGDGDF
Sbjct: 1113 QARDQVRLQAHGSIIILIGLPNFLHYFLLGPATILDGPLHSDGPLRVVKGKVLQRGDGDF 934

Query: 559 CLGILLYLLQVPSFLANETPYKVIMGQDLQGNLVSFRFVLSLFMHNLDHLTSGGAALRG 380
CLGILLYLLQVPSFLANETPYKVIMGQDLQGNLVSFRFVLSLFMHNLDHLTSGGAALRG
Sbjct: 933 CLGILLYLLQVPSFLANETPYKVIMGQDLQGNLVSFRFVLSLFMHNLDHLTSGGAALRG 754

Query: 379 GVHTDGGFFSCTCVLLPMHVYLGLGLFCDVADGGPLLANNNGTHILGGHQEPKGDVHLLLLLG 200
GVHTDGGFFSCTCVLLPMHVYLGLGLFCDVADGGPLLANNNGTHILGGHQEPKGDVHLLLLLG
Sbjct: 753 GVHTDGGFFSCTCVLLPMHVYLGLGLFCDVADGGPLLANNNGTHILGGHQEPKGDVHLLLLLG 574

Query: 199 WGPRCHR*ALAGLTTPRAKAPSAPILRSLCYLLIGDVGDLQGMVLQLVAIQLHDGSPG 29
WGPRCHR*ALAGLTTPRAKAPSAPILRSLCYLLIGDVGDLQGMVLQLVAIQLHDG PG
Sbjct: 573 WGPRCHR*ALAGLTTPRAKAPSAPILRSLCYLLIGDVGDLQGMVLQLVAIQLHDGLPG 403

Score = 529 bits (1150), Expect(3) = 0.0
Identities = 226/227 (99%), Positives = 226/227 (99%)
Frame = +2 / +1

Query: 32 RGAIMKLNQHLENHALKVSYPDEQIAQGPENGRGGFGSRGQPRQGSPPVAAGAPAKQQ 211
R AIMKLNQHLENHALKVSYPDEQIAQGPENGRGGFGSRGQPRQGSPPVAAGAPAKQQ
Sbjct: 406 RQAIMKLNQHLENHALKVSYPDEQIAQGPENGRGGFGSRGQPRQGSPPVAAGAPAKQQ 585

Query: 212 QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 391
QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG
Sbjct: 586 QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 765

Query: 392 CSSACKMILEIMHKEAKDTKTADEVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITI 571
CSSACKMILEIMHKEAKDTKTADEVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITI
Sbjct: 766 CSSACKMILEIMHKEAKDTKTADEVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITI 945

Query: 572 SSLQDLTLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS 712
SSLQDLTLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS
Sbjct: 946 SSLQDLTLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS 1086

Score = 512 bits (1113), Expect(3) = 0.0
Identities = 204/208 (98%), Positives = 204/208 (98%)
Frame = -2 / -2

Query: 1707 FKT*RKIFYSSH*GVIHPLGGAWRASLNNPRLKVPCAXISDTPRGXQCWANWVGWVG*XI 1528
FKT*RKIFYSSH*GVIHPLGGAWRASLNNPRLKVPCA ISDTPRG QCWANWVGWVG* I
Sbjct: 2087 FKT*RKIFYSSH*GVIHPLGGAWRASLNNPRLKVPCARISDTPRGRQCWANWVGWVG*EI 1908

Query: 1527 RVPHWNIFLNQVGKPDLPQGPXVPDSHSFSGLPGRAHSRFLPVVVLDSKGQGGAGHFLRA 1348
RVPHWNIFLNQVGKPDLPQGP VPDSHSFSGLPGRAHSRFLPVVVLDSKGQGGAGHFLRA
Sbjct: 1907 RVPHWNIFLNQVGKPDLPQGPVVPDSHSFSGLPGRAHSRFLPVVVLDSKGQGGAGHFLRA 1728

Query: 1347 WAWLLCPF*CCCLTWARMSRIFR*AI*LA*KCPMIFTMTWSFSSGVWSLGTTSAAVKFC 1168
WAWLLCPF*CCCLTWARMSRIFR*AI*LA*KCPMIFTMTWSFSSGVWSLGTTSAAVKFC
Sbjct: 1727 WAWLLCPF*CCCLTWARMSRIFR*AI*LA*KCPMIFTMTWSFSSGVWSLGTTSAAVKFC 1548

Query: 1167 NSFTVPPLPMTRPAADAGTRMWSSFT 1084
NSFTVPPLPMTRPAADAGTRMWSSFT
Sbjct: 1547 NSFTVPPLPMTRPAADAGTRMWSSFT 1464

Score = 504 bits (1094), Expect(3) = 0.0
Identities = 194/194 (100%), Positives = 194/194 (100%)
Frame = +1 / +3

Query: 715 SPDPWPEPGCCRSFSPFIQRSPAASQORYWGCSL*LLYAGSRAGDGAGVYPRPGSGRHRH 894
SPDPWPEPGCCRSFSPFIQRSPAASQORYWGCSL*LLYAGSRAGDGAGVYPRPGSGRHRH
Sbjct: 1095 SPDPWPEPGCCRSFSPFIQRSPAASQORYWGCSL*LLYAGSRAGDGAGVYPRPGSGRHRH 1274

Query: 895 QEGAAHQ TALPVCQRLHQDCTTRNT*LQSSYGYHHWTARGPIQSGKNLWQTQGGELLWS 1074
QEGAAHQ TALPVCQRLHQDCTTRNT*LQSSYGYHHWTARGPIQSGKNLWQTQGGELLWS
Sbjct: 1275 QEGAAHQ TALPVCQRLHQDCTTRNT*LQSSYGYHHWTARGPIQSGKNLWQTQGGELLWS 1454

Query: 1075 QGGSEAGDPHTCASISSWPGHWQRWKNGERVAEFDGS*GGSTKRDPD**ERPGHRENHRT 1254
QGGSEAGDPHTCASISSWPGHWQRWKNGERVAEFDGS*GGSTKRDPD**ERPGHRENHRT
Sbjct: 1455 QGGSEAGDPHTCASISSWPGHWQRWKNGERVAEFDGS*GGSTKRDPD**ERPGHRENHRT 1634

Query: 1255 FLCQSDGSTEDPRH 1296
FLCQSDGSTEDPRH
Sbjct: 1635 FLCQSDGSTEDPRH 1676

Score = 485 bits (1054), Expect(6) = 0.0
Identities = 197/213 (92%), Positives = 197/213 (92%)
Frame = -1 / -1

Query: 1513 EHLSQSSGQT*STARPCPGFPLILRPAGESTLSISARCCPGLXGTGRGWSLPPCXXXXX 1334
EHLSQSSGQT*STARPCPGFPLILRPAGESTLSISARCCPGL GTGRGWSLPPC
Sbjct: 1893 EHLSQSSGQT*STARPCPGFPLILRPAGESTLSISARCCPGLGTGRGWSLPPCLGLVT 1714

Query: 1333 XXXXXXXXXXXLQGDVSDLP LSHLTGIEMSDDFHD DLVVLIRGLVSWYYHLSCRQILQLVHR 1154
LQGDVSDLP LSHLTGIEMSDDFHD DLVVLIRGLVSWYYHLSCRQILQLVHR
Sbjct: 1713 LSLMLLLNLQGDVSDLP LSHLTGIEMSDDFHD DLVVLIRGLVSWYYHLSCRQILQLVHR 1534

Query: 1153 FSTFANDPASC*CWHTYVGLQLHFLLGTKEVLLLEFAIDSSLSLELGLWRSSDDNHTNFG 974
FSTFANDPASC*CWHTYVGLQLHFLLGTKEVLLLEFAIDSSLSLELGLWRSSDDNHTNFG
Sbjct: 1533 FSTFANDPASC*CWHTYVGLQLHFLLGTKEVLLLEFAIDSSLSLELGLWRSSDDNHTNFG 1354

Query: 973 VRCFGWCNLDGGAGKPGELFDVLP LLADDGAHC 875
VRCFGWCNLDGGAGKPGELFDVLP LLADDGAHC
Sbjct: 1353 VRCFGWCNLDGGAGKPGELFDVLP LLADDGAHC 1255

Score = 396 bits (858), Expect(4) = 0.0
Identities = 169/179 (94%), Positives = 169/179 (94%)
Frame = -2 / -2

Query: 711 LMAATSFS*ASRTFFIISCSALQQFSMAPFTVMVLSGL*RVRSCNEEMVIFVSVSCSTFF 532
LMAATSFS*ASRTFFIISCSALQQFSMAPFTVMVLSGL*RVRSCNEEMVIFVSVSCSTFF
Sbjct: 1085 LMAATSFS*ASRTFFIISCSALQQFSMAPFTVMVLSGL*RVRSCNEEMVIFVSVSCSTFF 906

Query: 531 RFRPSLPMRPTKLLWARIFRGTXXXXXXXXXXXLCIISKIILQAEQPSGVECTLMAFSA 352
RFRPSLPMRPTKLLWARIFRGTX LCIISKIILQAEQPSGVECTLMAFSA
Sbjct: 905 RFRPSLPMRPTKLLWARIFRGTTSSAVLVSLASLCIISKIILQAEQPSGVECTLMAFSA 726

Query: 351 APAFSFLCTSILDWVCFVMLRMVAPSLPIMAPTYWVGTRSRMGSTCCCLAGAPAAATGE 175
APAFSFLCTSILDWVCFVMLRMVAPSLPIMAPTYWVGTRSRMGSTCCCLAGAPAAATGE
Sbjct: 725 APAFSFLCTSILDWVCFVMLRMVAPSLPIMAPTYWVGTRSRMGSTCCCLAGAPAAATGE 549

Score = 269 bits (582), Expect(6) = 0.0
Identities = 113/134 (84%), Positives = 113/134 (84%)
Frame = -3 / -3

Query: 701 PHHSHRPPELSSLFPARPCNNSRXXXXXXXXXXQGCKG*GLATTRW*FLSRYLALPSSGSV 522
PHHSHRPPELSSLFPARPCNNSR QGCKG*GLATTRW*FLSRYLALPSSGSV
Sbjct: 1075 PHHSHRPPELSSLFPARPCNNSRWPPSQ*WSSQGCKG*GLATTRW*FLSRYLALPSSGSV 896

Query: 521 LPCQ*DALSYYGPGSSGEPRQPFWCP*PLYAXXXXXXXXXXXXXPQGWSAH*WLFQLHLR 342
LPCQ*DALSYYGPGSSGEPRQPFWCP*PLYA PQGWSAH*WLFQLHLR
Sbjct: 895 LPCQ*DALSYYGPGSSGEPRQPFWCP*PLYA*SPRSSYKRRSSPQGWSAH*WLFQLHLR 716

Query: 341 SPSYARLSWTGSVL 300
SPSYARLSWTGSVL
Sbjct: 715 SPSYARLSWTGSVL 674

Score = 258 bits (557), Expect(3) = 0.0
Identities = 109/112 (97%), Positives = 109/112 (97%)
Frame = +1 / +3

Query: 1372 SLXLVQDNNNGQKSRVCSRPQA*E*VGIRDTWAGL*IRFAHLIEKDVPVRNPDLAPNTH 1551
SLSL VQDNNNGQKSRVCSRPQA*E*VGIRDTWAGL*IRFAHLIEKDVPVRNPDLAPNTH
Sbjct: 1752 SLXLVQDNNNGQKSRVCSRPQA*E*VGIRDTWAGL*IRFAHLIEKDVPVRNPDLAPNTH 1931

Query: 1552 PIGPTLXAPRGVRNXSARHF*TWIV*RSSPGPTKRDHTSVGRKIKFPSGFK 1707
PIGPTL APRGVRN SARHF*TWIV*RSSPGPTKRDHTSVGRKIKFPSGFK
Sbjct: 1932 PIGPTLSAPRGVRNSSARHF*TWIV*RSSPGPTKRDHTSVGRKIKFPSGFK 2087

Score = 248 bits (535), Expect(3) = 0.0
Identities = 102/103 (99%), Positives = 103/103 (100%)
Frame = -2 / -2

Query: 1020 NWASGGPVMITIRTLESGVSGGAILMEALANRESCLMCCPFLPMMAPTAWAGINTCTISC 841
NWASGGPVMITIRTLESGVSGGAILMEALANRESCLMCCPFLPMMAPTAWAGINTCTISC
Sbjct: 1400 NWASGGPVMITIRTLESGVSGGAILMEALANRESCLMCCPFLPMMAPTAWAGINTCTISC 1221

Query: 840 SGACIKEL*GAAPVTLLGGGGTALDEAGKRPTAARFRPGIR*E 712
SGACIKEL*GAAPVTLLGGGGTALDEAGKRPTAARFRPGIR*+
Sbjct: 1220 SGACIKEL*GAAPVTLLGGGGTALDEAGKRPTAARFRPGIR*D 1092

Score = 230 bits (496), Expect(4) = 0.0
Identities = 99/99 (100%), Positives = 99/99 (100%)
Frame = +3 / +2

Query: 414 SWRLCIKRLRTPKRLTRFP*RSWPIITL*GVSLARKDGT*RR*SKIPRQKSPSPRCKTLP 593
SWRLCIKRLRTPKRLTRFP*RSWPIITL*GVSLARKDGT*RR*SKIPRQKSPSPRCKTLP
Sbjct: 788 SWRLCIKRLRTPKRLTRFP*RSWPIITL*GVSLARKDGT*RR*SKIPRQKSPSPRCKTLP 967

Query: 594 FTTLRGPSL*RGPSRIVAGPSRK**RKFG RPMRMMWLP* 710
FTTLRGPSL*RGPSRIVAGPSRK**RKFG RPMRMMWLP*
Sbjct: 968 FTTLRGPSL*RGPSRIVAGPSRK**RKFG RPMRMMWLP* 1084

Score = 223 bits (482), Expect(5) = 0.0
Identities = 88/88 (100%), Positives = 88/88 (100%)
Frame = +3 / +2

Query: 114 HRDLRMGAEGALALGVSPARAHLWQRGPQPSSSKWTSPPFGSWCPPSMWVPLLARRGPPSA 293
HRDLRMGAEGALALGVSPARAHLWQRGPQPSSSKWTSPPFGSWCPPSMWVPLLARRGPPSA
Sbjct: 488 HRDLRMGAEGALALGVSPARAHLWQRGPQPSSSKWTSPPFGSWCPPSMWVPLLARRGPPSA 667

Query: 294 TSQNRPSPR*TCIGRRTQVQLKKPSVCT 377
TSQNRPSPR*TCIGRRTQVQLKKPSVCT
Sbjct: 668 TSQNRPSPR*TCIGRRTQVQLKKPSVCT 751

Score = 196 bits (422), Expect(5) = 0.0
Identities = 78/78 (100%), Positives = 78/78 (100%)
Frame = +1 / +3

Query: 424 YA*RG*GHQNG*RGSPEDPGP**LCRASHWQGRTEPEEGRARYRDKNHLLVARPYPLQP 603
YA*RG*GHQNG*RGSPEDPGP**LCRASHWQGRTEPEEGRARYRDKNHLLVARPYPLQP
Sbjct: 798 YA*RG*GHQNG*RGSPEDPGP**LCRASHWQGRTEPEEGRARYRDKNHLLVARPYPLQP 977

Query: 604 *EDHHCEGGHRELLQGRA 657
*EDHHCEGGHRELLQGRA
Sbjct: 978 *EDHHCEGGHRELLQGRA 1031

Score = 132 bits (282), Expect(4) = 0.0
Identities = 50/55 (90%), Positives = 50/55 (90%)
Frame = +1 / +3

Query: 19 PQFTPGSHHEAEWPPVGEPCPEGLLHPR*ADSTGT*EWAPRGLWLSGSAPPGLTC 183
P SHHEAEWPPVGEPCPEGLLHPR*ADSTGT*EWAPRGLWLSGSAPPGLTC
Sbjct: 393 PGADQASHHEAEWPPVGEPCPEGLLHPR*ADSTGT*EWAPRGLWLSGSAPPGLTC 557

Score = 125 bits (268), Expect(4) = 0.0
Identities = 45/45 (100%), Positives = 45/45 (100%)
Frame = +1 / +3

Query: 250 VCGCHYWQGGGHHHPQHHTDPVQDRRA*EGERRCS*KSHQCALHP 384
VCGCHYWQGGGHHHPQHHTDPVQDRRA*EGERRCS*KSHQCALHP
Sbjct: 624 VCGCHYWQGGGHHHPQHHTDPVQDRRA*EGERRCS*KSHQCALHP 758

Score = 115 bits (245), Expect(6) = 0.0
Identities = 46/48 (95%), Positives = 46/48 (95%)
Frame = -1 / -1

Query: 1708 F*NLKEILFFFPLRCDPPSWWGLESTFKSALRXNF*HPEGXTV 1565
F*NLKEILFFFPLRCDPPSWWGLESTFKSALR NF*HPEG TV
Sbjct: 2088 F*NLKEILFFFPLRCDPPSWWGLESTFKSALR*NF*HPEGQTV 1945

Score = 86.3 bits (182), Expect(4) = 0.0
Identities = 36/36 (100%), Positives = 36/36 (100%)
Frame = -1 / -1

Query: 820 AIGSSPSNAAGRRRDCAG*SWEKTYSSQVQARDQVR 713
AIGSSPSNAAGRRRDCAG*SWEKTYSSQVQARDQVR
Sbjct: 1200 AIGSSPSNAAGRRRDCAG*SWEKTYSSQVQARDQVR 1093

Score = 85.4 bits (180), Expect(4) = 0.0
Identities = 31/31 (100%), Positives = 31/31 (100%)
Frame = -2 / -2

Query: 129 FSGPCAICSSGM*ETFRAWFSNWWPFSFMMA 37
FSGPCAICSSGM*ETFRAWFSNWWPFSFMMA
Sbjct: 503 FSGPCAICSSGM*ETFRAWFSNWWPFSFMMA 411

Score = 81.2 bits (171), Expect(6) = 0.0
Identities = 35/49 (71%), Positives = 35/49 (71%)
Frame = -3 / -3

Query: 182 QVSPGGADPESQSPLGAHSQVPVLSAHRGCRRXXXXXXXXXXXXXXXXXX*WL 36
QVSPGGADPESQSPLGAHSQVPVLSAHRGCRR *WL
Sbjct: 556 QVSPGGADPESQSPLGAHSQVPVLSAHRGCRRPSGHGSPTGGHSAS*WL 410

Score = 56.5 bits (117), Expect(6) = 0.0
Identities = 21/21 (100%), Positives = 21/21 (100%)
Frame = -3 / -3

Query: 809 QPQ*RCWEAAGLRWMKLGKDL 747
QPQ*RCWEAAGLRWMKLGKDL
Sbjct: 1189 QPQ*RCWEAAGLRWMKLGKDL 1127

Score = 42.8 bits (87), Expect(2) = 2e-06
Identities = 13/37 (35%), Positives = 26/37 (70%)
Frame = +2 / +1

Query: 218 DIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDV 328
++PL++L +VG +IGKEG ++ + + T++KI +
Sbjct: 835 EVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITI 945

Score = 42.8 bits (87), Expect(2) = 2e-06
Identities = 13/37 (35%), Positives = 26/37 (70%)
Frame = +2 / +1

Query: 461 EVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITI 571
++PL++L +VG +IGKEG ++ + + T++KI +
Sbjct: 592 DIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDV 702

Score = 40.9 bits (83), Expect(2) = 2e-06
Identities = 13/44 (29%), Positives = 26/44 (59%)
Frame = +2 / +1

Query: 863 IPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVI 994
+PA A G +IGK G+ + +L +A + + +TPD ++++
Sbjct: 1489 VPASAAGRVIIGKGGKTVNELQNLTAEEVVPRDQTPDENDQVIV 1620

Score = 40.9 bits (83), Expect(2) = 2e-06
Identities = 13/44 (29%), Positives = 26/44 (59%)
Frame = +2 / +1

Query: 1109 VPASAAGRVIIGKGGKTVNELQNLTAEEVVPRDQTPDENDQVIV 1240
+PA A G +IGK G+ + +L +A + + +TPD ++++
Sbjct: 1243 IPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVI 1374

Score = 38.6 bits (78), Expect = 6.8
Identities = 15/54 (27%), Positives = 30/54 (55%)
Frame = +2 / +1

Query: 227 LRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPE 388
+++ +P Q VGAIIGK+G I+ +++ + I + E + + + + PE
Sbjct: 1231 VQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPE 1392

Score = 38.6 bits (78), Expect = 6.8
Identities = 15/54 (27%), Positives = 30/54 (55%)
Frame = +2 / +1

Query: 851 VQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPE 1012
+++ +P Q VGAIIGK+G I+ +++ + I + E + + + + PE
Sbjct: 601 LRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPE 762

Score = 35.4 bits (71), Expect(6) = 0.0
Identities = 11/11 (100%), Positives = 11/11 (100%)
Frame = -3 / -3

Query: 260 HPHTGWAPGAE 228
HPHTGWAPGAE
Sbjct: 634 HPHTGWAPGAE 602

Score = 30.4 bits (60), Expect(5) = 0.0
Identities = 12/13 (92%), Positives = 13/13 (100%)
Frame = +3 / +2

Query: 30 PGEPS*S*MATSW 68
PG+PS*S*MATSW
Sbjct: 404 PGKPS*S*MATSW 442

Score = 26.7 bits (52), Expect(5) = 0.0
Identities = 11/11 (100%), Positives = 11/11 (100%)
Frame = +3 / +2

Query: 747 *VFSQLHPAQS 779
*VFSQLHPAQS
Sbjct: 1127 *VFSQLHPAQS 1159

>gi|21361351|ref|NM_006546.2| Homo sapiens IGF-II mRNA-binding protein 1 (IM)
Length = 2381

Score = 576 bits (1252), Expect(3) = 0.0
Identities = 251/279 (89%), Positives = 253/279 (90%)
Frame = +2 / +3

Query: 704 AMSSHLIPGLNLAAGVLFXXXXXXXXXXXXXXXXXTGAAPYSSFMQAPEQEMVQVFIPAQAVG 883
++ SHL PGLNLAAGVLF TGAAPYSSFMQAPEQEMVQVFIPAQAVG
Sbjct: 1380 SLQSHLTPGLNLAAGVLFPASSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVG 1559

Query: 884 AIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEEN 1063
AIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEEN
Sbjct: 1560 AIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEEN 1739

Query: 1064 FFGPKKEEVKLETHIRVPASAAGRVIKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVK 1243
FFGPKKEEVKLETHIRVPASAAGRVIKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVK
Sbjct: 1740 FFGPKKEEVKLETHIRVPASAAGRVIKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVK 1919

Query: 1244 IIGHFYASQMAQRKIRDILAQVKQHQKQSNQAQARRKXXXXXXXXXESRTTTGRNRECA 1423
IIGHFYASQMAQRKIRDILAQVKQHQKQSNQAQARRK ESRTTTGRNRECA
Sbjct: 1920 IIGHFYASQMAQRKIRDILAQVKQHQKQSNQAQARRK*PAPPCPFESRTTTGRNRECA 2099

Query: 1424 LPGRPENEWESGTXGPGCRSGLPT*LRKMFQ*GTLIXQP 1540
LPGRPENEWESGT GPGCRSGLPT*LRKMFQ*GTLI QP
Sbjct: 2100 LPGRPENEWESGTPGPGCRSGLPT*LRKMFQ*GTLISQP 2216

Score = 555 bits (1206), Expect(4) = 0.0
Identities = 227/237 (95%), Positives = 232/237 (97%)
Frame = -1 / -1

Query: 739 QVQARDQVRAHGSHIILIGLPNLFHYFLLGPATILDGPHLSDGPLRVVKGKVLQRGDGDF 560
Q + + +++AHGSHIILIGLPNLFHYFLLGPATILDGPHLSDGPLRVVKGKVLQRGDGDF
Sbjct: 1409 QARGQVRLQAHGSHIILIGLPNLFHYFLLGPATILDGPHLSDGPLRVVKGKVLQRGDGDF 1230

Query: 559 CLGILLYLLQVPSFLANETPYKVMGQDLQGNLVSFRGVLSLFMHNLQDHLTSGGAALRG 380
 CLGILLYLLQVPSFLANETPYKVMGQ LQGNLVSFRGVLSLFMHNLQDHLTSGGAALRG
 Sbjct: 1229 CLGILLYLLQVPSFLANETPYKVMGQDLQGNLVSFRGVLSLFMHNLQDHLTSGGAALRG 1050

Query: 379 GVHTDGGFFSCTCVLLPMHVYLGLGLFCDVADGGPLLANNGTHILGGHQEPKGDVHLLLLG 200
 GVHTDGGFFSCTCVLLPMHVYLGLGLFCDVADGGPLLANNGTHILGGHQEPKGDVHLLLLG
 Sbjct: 1049 GVHTDGGFFSCTCVLLPMHVYLGLGLFCDVADGGPLLANNGTHILGGHQEPKGDVHLLLLG 870

Query: 199 WGPRCHR*ALAGLTPRAKAPSAPILRSLCYLLIGDVGD LQGMVLQLVAIQLHDGSPG 29
 WGPRCHR*ALAGLTPRAKAPSAPILRSLCYLLIGDVGD LQGMVLQLVAIQLHDG PG
 Sbjct: 869 WGPRCHR*ALAGLTPRAKAPSAPILRSLCYLLIGDVGD LQGMVLQLVAIQLHDGLPG 699

Score = 527 bits (1145), Expect(3) = 0.0
 Identities = 225/227 (99%), Positives = 225/227 (99%)
 Frame = +2 / +3

Query: 32 RGAIMKLNQHLENHALKVSYPDEQIAQGPENRRGGFGSRGQPRQGSPVAAGAPAKQQ 211
 R AIMKLNQHLENHALKVSYPDEQIAQGPENRRGGFGSRGQPRQGSPVAAGAPAKQQ
 Sbjct: 702 RGAIMKLNQHLENHALKVSYPDEQIAQGPENRRGGFGSRGQPRQGSPVAAGAPAKQQ 881

Query: 212 QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKASVHSTPEG 391
 QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKASVHSTPEG
 Sbjct: 882 QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKASVHSTPEG 1061

Query: 392 CSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRIGKEGRNLKKVEQDTETKITI 571
 CSSACKMILEIMHKEAKDTKTADDEVPLK LAHNNFVGRIGKEGRNLKKVEQDTETKITI
 Sbjct: 1062 CSSACKMILEIMHKEAKDTKTADDEVPLKTLAHNNFVGRIGKEGRNLKKVEQDTETKITI 1241

Query: 572 SSLQDLTLYNPRTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS 712
 SSLQDLTLYNPRTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS
 Sbjct: 1242 SSLQDLTLYNPRTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS 1382

Score = 522 bits (1133), Expect(5) = 0.0
 Identities = 218/242 (90%), Positives = 220/242 (90%)
 Frame = -3 / -3

Query: 1583 PRGAXSVGPIGWVFGAXRSGFLTGTSTFSIKWANLIYSPAXVSRIPTHSQACRGEHTLDFC 1404
 P G +G +G GA RSGFLTGTSTFSIKWANLIYSPA VSRIPTHSQACRGEHTLDFC
 Sbjct: 2259 PEGQTVLGLGRCLGAERSGFLTGTSTFSIKWANLIYSPAQVSRIPTHSQACRGEHTLDFC 2080

Query: 1403 PLLSWTXRDREGLVTXXXXXXXXXXXXSDAAA*PGPGCLGSSVEPSDWHNRNVR*FSR*PGR 1224
 PLLSWT RDREGLVT SDAAA*PGPGCLGSSVEPSDWHNRNVR*FSR*PGR
 Sbjct: 2079 PLLSWTRRDREGLVTSFVPGPGYSVPSDAAA*PGPGCLGSSVEPSDWHNRNVR*FSR*PGR 1900

Query: 1223 SHQSGLLVLPPQLPSNSATRSPPFHLCQ*PGQLMLAHVCGSPASLPPWDQRSSPP*VC 1044
 SHQSGLLVLPPQLPSNSATRSPPFHLCQ*PGQLMLAHVCGSPASLPPWDQRSSPP*VC
 Sbjct: 1899 SHQSGLLVLPPQLPSNSATRSPPFHLCQ*PGQLMLAHVCGSPASLPPWDQRSSPP*VC 1720

Query: 1043 HRFFPEP*IGPLAVQ***PYELWSQVFRVVQS*WRRWQTGRAV*CAAPSCR*WRPLPGRG 864
 HRFFPEP*IGPLAVQ***PYELWSQVFRVVQS*WRRWQTGRAV*CAAPSCR*WRPLPGRG
 Sbjct: 1719 HRFFPEP*IGPLAVQ***PYELWSQVFRVVQS*WRRWQTGRAV*CAAPSCR*WRPLPGRG 1540

Query: 863 *T 858
*T
Sbjct: 1539 *T 1534

Score = 510 bits (1108), Expect(6) = 0.0
Identities = 210/225 (93%), Positives = 210/225 (93%)
Frame = +3 / +1

Query: 837 PSRRWCRCCLSPPRQWAPXXXXXXXXXXXXPGLPAPPSRLHHPKHLTPKFVWLSSLDRQRP 1016
PSRRWCRCCLSPPRQWAP PGLPAPPSRLHHPKHLTPKFVWLSSLDRQRP
Sbjct: 1513 PSRRWCRCCLSPPRQWAPSSARRGSTSNSSPGLPAPPSRLHHPKHLTPKFVWLSSLDRQRP 1692

Query: 1017 NSRLREESMANSRRRTSLVPRRK*SWRPTYVCQHQQLAGSLAKVEKR*TSCRI*RQLRW* 1196
NSRLREESMANSRRRTSLVPRRK*SWRPTYVCQHQQLAGSLAKVEKR*TSCRI*RQLRW*
Sbjct: 1693 NSRLREESMANSRRRTSLVPRRK*SWRPTYVCQHQQLAGSLAKVEKR*TSCRI*RQLRW* 1872

Query: 1197 YQETRPLMRTTRSS*KSSDISMPVRWLNGRSETSWPRLSSSIRRDVTRPRHGGSDQPLP 1376
YQETRPLMRTTRSS*KSSDISMPVRWLNGRSETSWPRLSSSIRRDVTRPRH GSDQPLP
Sbjct: 1873 YQETRPLMRTTRSS*KSSDISMPVRWLNGRSETSWPRLSSSIRRDVTRPRHEGSDQPLP 2052

Query: 1377 VPXSPGQQRAEIESVLSPAGLRMSGNPGHXGRAVDQVCPLD*ERC 1511
VP SPGQQRAEIESVLSPAGLRMSGNPGH GRAVDQVCPLD*ERC
Sbjct: 2053 VPSSPGQQRAEIESVLSPAGLRMSGNPGHLGRAVDQVCPLD*ERC 2187

Score = 504 bits (1094), Expect(5) = 0.0
Identities = 194/194 (100%), Positives = 194/194 (100%)
Frame = +1 / +2

Query: 715 SPDPWPEPGCCRSFPSFIQSPAASQQRYWGCSL*LLYAGSRAGDGAGVYPRPGSGRHHR 894
SPDPWPEPGCCRSFPSFIQSPAASQQRYWGCSL*LLYAGSRAGDGAGVYPRPGSGRHHR
Sbjct: 1391 SPDPWPEPGCCRSFPSFIQSPAASQQRYWGCSL*LLYAGSRAGDGAGVYPRPGSGRHHR 1570

Query: 895 QEGAAHQ TALPVCQRLHQDCTTRNT*LQSSYGYHHWTARGPIQGSGKNLWQTQGGELLWS 1074
QEGAAHQ TALPVCQRLHQDCTTRNT*LQSSYGYHHWTARGPIQGSGKNLWQTQGGELLWS
Sbjct: 1571 QEGAAHQ TALPVCQRLHQDCTTRNT*LQSSYGYHHWTARGPIQGSGKNLWQTQGGELLWS 1750

Query: 1075 QGGSEAGDPHTCASISSWPQHWQRWKNGERVAEFDGS*GGSTKRDPD**ERPGHRENHRT 1254
QGGSEAGDPHTCASISSWPQHWQRWKNGERVAEFDGS*GGSTKRDPD**ERPGHRENHRT
Sbjct: 1751 QGGSEAGDPHTCASISSWPQHWQRWKNGERVAEFDGS*GGSTKRDPD**ERPGHRENHRT 1930

Query: 1255 FLCQSDGSTEDPRH 1296
FLCQSDGSTEDPRH
Sbjct: 1931 FLCQSDGSTEDPRH 1972

Score = 482 bits (1046), Expect(6) = 0.0
Identities = 196/213 (92%), Positives = 196/213 (92%)
Frame = -1 / -1

Query: 1513 EHLSQSSGQT*STARPCPGFPLILRPAGESTLSISARCCPGLXGTGRGWSLPPCXXXXX 1334
EHLSQSSGQT*STARPCPGFPLILRPAGESTLSISARCCPGL GTGRGWSLP C
Sbjct: 2189 EHLSQSSGQT*STARPCPGFPLILRPAGESTLSISARCCPGLGTGRGWSLPSCLGLVT 2010

Query: 1333 XXXXXXXXXLGQDVSDLP LSHLTGIEMSDDFHDDL VVLIRGLVSWYYHLSCRQILQLVHR 1154
LGQDVSDLP LSHLTGIEMSDDFHDDL VVLIRGLVSWYYHLSCRQILQLVHR
Sbjct: 2009 LSLMLLLNLGQDVSDLP LSHLTGIEMSDDFHDDL VVLIRGLVSWYYHLSCRQILQLVHR 1830

Query: 1153 FSTFANDPASC*CWHTYVGLQLHFL LGTKEVLLLEFAIDSSLSLELGLWRSSDDNHTNFG 974
FSTFANDPASC*CWHTYVGLQLHFL LGTKEVLLLEFAIDSSLSLELGLWRSSDDNHTNFG
Sbjct: 1829 FSTFANDPASC*CWHTYVGLQLHFL LGTKEVLLLEFAIDSSLSLELGLWRSSDDNHTNFG 1650

Query: 973 VRCFGWCNLDGGAGKPGELFDVLP LLADDGAHC 875
VRCFGWCNLDGGAGKPGELFDVLP LLADDGAHC
Sbjct: 1649 VRCFGWCNLDGGAGKPGELFDVLP LLADDGAHC 1551

Score = 395 bits (857), Expect(5) = 0.0
Identities = 168/179 (93%), Positives = 169/179 (94%)
Frame = -2 / -2

Query: 711 LMAATSFS*ASRTFFIISCSALQQFS MAPFTVMVLSGL*RVRSCNEEMVIFVSVSCSTFF 532
LMAATSFS*ASRTFFIISCSALQQFS MAPFTVMVLSGL*RVRSCNEEMVIFVSVSCSTFF
Sbjct: 1381 LMAATSFS*ASRTFFIISCSALQQFS MAPFTVMVLSGL*RVRSCNEEMVIFVSVSCSTFF 1202

Query: 531 RFRPSLPMRRPTKLLWARIFRG TXXXXXXXXXXLCIISKIILQAEQPSGVECTLMAFSA 352
RFRPSLPMRRPTKLLWAR+FRGT LCIISKIILQAEQPSGVECTLMAFSA
Sbjct: 1201 RFRPSLPMRRPTKLLWARVFRGTSSAVLVSLASLCIISKIILQAEQPSGVECTLMAFSA 1022

Query: 351 APAFSFLCTSILDWVCFVMLRMVAPSLPIMAPTYWVGTRSR RGMSTCCCLAGAPAAATGE 175
APAFSFLCTSILDWVCFVMLRMVAPSLPIMAPTYWVGTRSR RGMSTCCCLAGAPAAATGE
Sbjct: 1021 APAFSFLCTSILDWVCFVMLRMVAPSLPIMAPTYWVGTRSR RGMSTCCCLAGAPAAATGE 845

Score = 374 bits (810), Expect(4) = 0.0
Identities = 150/152 (98%), Positives = 150/152 (98%)
Frame = -2 / -2

Query: 1539 G*XIRVPHWNIFLNQVGKPDLP GPXVPD SHSFSGLP GRAHSRFLPVVVLDSKGQGGAGH 1360
G* IRVPHWNIFLNQVGKPDLP GP VPDSHSFSGLP GRAHSRFLPVVVLDSKGQGGAGH
Sbjct: 2215 G*EIRVPHWNIFLNQVGKPDLP GP GPVDPD SHSFSGLP GRAHSRFLPVVVLDSKGQGGAGH 2036

Query: 1359 FLRAWAWLLCPF*CCCLTWARMSRIFR*AI*LA*KCPMIFTMTWSFSSGVWSLGT TTSAA 1180
FLRAWAWLLCPF*CCCLTWARMSRIFR*AI*LA*KCPMIFTMTWSFSSGVWSLGT TTSAA
Sbjct: 2035 FLRAWAWLLCPF*CCCLTWARMSRIFR*AI*LA*KCPMIFTMTWSFSSGVWSLGT TTSAA 1856

Query: 1179 VKFCNSFTVFPPLPMTRPAADAGTRMWVSSFT 1084
VKFCNSFTVFPPLPMTRPAADAGTRMWVSSFT
Sbjct: 1855 VKFCNSFTVFPPLPMTRPAADAGTRMWVSSFT 1760

Score = 269 bits (582), Expect(6) = 0.0
Identities = 113/134 (84%), Positives = 113/134 (84%)
Frame = -3 / -3

Query: 701 PHHSHRPPELSSLF PARPCNSRXXXXXXXXXQGCKG*GLATRRW*FLSRYLALPSSGSV 522
PHHSHRPPELSSLF PARPCNSR QGCKG*GLATRRW*FLSRYLALPSSGSV
Sbjct: 1371 PHHSHRPPELSSLF PARPCNSRWPPSQ*WSSQGCKG*GLATRRW*FLSRYLALPSSGSV 1192

Query: 521 LPCQ*DALQSYYPGSSGEPQPFWCP*PLYAXXXXXXXXXXXXXPQWSAH*WLFQLHLR 342
LPCQ*DALQSYYPGSSGEPQPFWCP*PLYA PQWSAH*WLFQLHLR
Sbjct: 1191 LPCQ*DALQSYYPGSSGEPQPFWCP*PLYA*SPRSSYKRRSSPQWSAH*WLFQLHLR 1012

Query: 341 SPSYARLSWTGSVL 300
SPSYARLSWTGSVL
Sbjct: 1011 SPSYARLSWTGSVL 970

Score = 247 bits (534), Expect(4) = 0.0
Identities = 101/103 (98%), Positives = 103/103 (100%)
Frame = -2 / -2

Query: 1020 NWASGGPVMITIRTLESVSGGAILMEALANRESCLMCCPFLPMMAPTAWAGINTCTISC 841
NWASGGPVMITIRTLESVSGGAILMEALANRESCLMCCPFLPMMAPTAWAGINTCTISC
Sbjct: 1696 NWASGGPVMITIRTLESVSGGAILMEALANRESCLMCCPFLPMMAPTAWAGINTCTISC 1517

Query: 840 SGACIKEL*GAAPVTLLGGGGTALDEAGKRPTAARFRPGIR*E 712
SGACIKEL*GAAPVTLLGGGGTALDEAGKRPTAARFRPG+R*+
Sbjct: 1516 SGACIKEL*GAAPVTLLGGGGTALDEAGKRPTAARFRPGVR*D 1388

Score = 227 bits (491), Expect(6) = 0.0
Identities = 98/99 (98%), Positives = 98/99 (98%)
Frame = +3 / +1

Query: 414 SWRLCIKRLRTPKRLTRFP*RSWPIITL*GVSLARKDGT*RR*SKIPRQKSPSPRCKTLP 593
SWRLCIKRLRTPKRLTRFP*R WPIITL*GVSLARKDGT*RR*SKIPRQKSPSPRCKTLP
Sbjct: 1084 SWRLCIKRLRTPKRLTRFP*RPWPIITL*GVSLARKDGT*RR*SKIPRQKSPSPRCKTLP 1263

Query: 594 FTTLRGPSL*RGPSRIVAGPSRK**RKFGPRMMMWLP* 710
FTTLRGPSL*RGPSRIVAGPSRK**RKFGPRMMMWLP*
Sbjct: 1264 FTTLRGPSL*RGPSRIVAGPSRK**RKFGPRMMMWLP* 1380

Score = 223 bits (482), Expect(5) = 0.0
Identities = 88/88 (100%), Positives = 88/88 (100%)
Frame = +3 / +1

Query: 114 HRDLRMGAEGALALGVSPARHLWQRGQPSSSKWTSFPGSWCPSMWVPLLARRGPPSA 293
HRDLRMGAEGALALGVSPARHLWQRGQPSSSKWTSFPGSWCPSMWVPLLARRGPPSA
Sbjct: 784 HRDLRMGAEGALALGVSPARHLWQRGQPSSSKWTSFPGSWCPSMWVPLLARRGPPSA 963

Query: 294 TSQNRPSPR*TCIGRRTQVQLKKPSVCT 377
TSQNRPSPR*TCIGRRTQVQLKKPSVCT
Sbjct: 964 TSQNRPSPR*TCIGRRTQVQLKKPSVCT 1047

Score = 196 bits (422), Expect(5) = 0.0
Identities = 78/78 (100%), Positives = 78/78 (100%)
Frame = +1 / +2

Query: 424 YA*RG*GHQNG*RGSPEDPGP**LCRASHWQGRTEPEEGRARYRDKNHLLVARPYPLQP 603
YA*RG*GHQNG*RGSPEDPGP**LCRASHWQGRTEPEEGRARYRDKNHLLVARPYPLQP
Sbjct: 1094 YA*RG*GHQNG*RGSPEDPGP**LCRASHWQGRTEPEEGRARYRDKNHLLVARPYPLQP 1273

Query: 604 *EDHHCEGGHRELLQGRA 657
*EDHHCEGGHRELLQGRA
Sbjct: 1274 *EDHHCEGGHRELLQGRA 1327

Score = 141 bits (303), Expect(4) = 0.0
Identities = 54/56 (96%), Positives = 54/56 (96%)
Frame = -2 / -1

Query: 1704 KT*RKFYFSSH*GVIHPLGGAWRASLNNPRLKVPCAXISDTPRGXQCWANWVGWVG 1537
KT*RKFYFSSH*GVIHPLGGAWRASLNNPRLKVPCA ISDTPRG QCWANWVGWVG
Sbjct: 2381 KT*RKFYFSSH*GVIHPLGGAWRASLNNPRLKVPCARISDTPRGRQCWANWVGWVG 2214

Score = 136 bits (291), Expect(5) = 0.0
Identities = 60/71 (84%), Positives = 60/71 (84%)
Frame = +1 / +2

Query: 1372 SLSLXVQDNNGQKSRVCSPRQA*E*VGIRDWAGL*IRFAHLIEKDVVRNPDL SAPNTH 1551
SLSL VQDNNGQKSRVCSPRQA*E*VGIRDWAGL*IRFAHLIEKDVVRNPDL SAP
Sbjct: 2048 SLSLRVQDNNGQKSRVCSPRQA*E*VGIRDWAGL*IRFAHLIEKDVVRNPDL SAPKHL 2227

Query: 1552 PIGPTLXAPRG 1584
P P P G
Sbjct: 2228 PNWPNTVCPSPG 2260

Score = 133 bits (284), Expect(3) = 0.0
Identities = 53/55 (96%), Positives = 53/55 (96%)
Frame = +2 / +1

Query: 1538 PQTPTQLAQHCXPLGVSEIXAQGTFRGLFKEALQAPPRGWITPQWEEK*NFLQV 1702
PQTPTQLAQHC PLGVSEI AQGTFRGLFKEALQAPPRGWITPQWEEK*NFLQV
Sbjct: 2215 PQTPTQLAQHCLPLGVSEILAQGTFRGLFKEALQAPPRGWITPQWEEK*NFLQV 2379

Score = 133 bits (284), Expect(6) = 0.0
Identities = 52/54 (96%), Positives = 52/54 (96%)
Frame = +3 / +2

Query: 1542 KHPPNWPNTVCPSPGCQKX*RKALLNVDCLKKLSRPHQEGGSHLSGKKNKISFRF 1703
KH PNWPNTVCPSPGCQK *RKALLNVDCLKKLSRPHQEGGSHLSGKKNKISFRF
Sbjct: 2219 KHLPNWPNTVCPSPGCQKF*RKALLNVDCLKKLSRPHQEGGSHLSGKKNKISFRF 2380

Score = 132 bits (282), Expect(6) = 0.0
Identities = 50/55 (90%), Positives = 50/55 (90%)
Frame = +1 / +2

Query: 19 PQFTPGSHHEAEWPPVGEPCPEGLLHPR*ADSTGT*EWAPRGLWLSGSAPPGLTC 183
P SHHEAEWPPVGEPCPEGLLHPR*ADSTGT*EWAPRGLWLSGSAPPGLTC
Sbjct: 689 PGADQASHHEAEWPPVGEPCPEGLLHPR*ADSTGT*EWAPRGLWLSGSAPPGLTC 853

Score = 129 bits (276), Expect(3) = 4e-38
Identities = 52/55 (94%), Positives = 53/55 (96%)
Frame = +1 / +3

Query: 1540 PNTHPIGPTLXAPRGVRNXSARHF*TWIV*RSSPGPTKRVDHTSVGRKIKFPSGF 1704
PNT+PIGPTL APRGVRN SARHF*TWIV*RSSPGPTKRVDHTSVGRKIKFPSGF
Sbjct: 2217 PNTYPIGPTLSAPRGVRNSSARHF*TWIV*RSSPGPTKRVDHTSVGRKIKFPSGF 2381

Score = 125 bits (268), Expect(6) = 0.0
Identities = 45/45 (100%), Positives = 45/45 (100%)
Frame = +1 / +2

Query: 250 VCGCHYWQGGGHHHPQHHKTDVPVQDRRA*EGERRCS*KSHQCALHP 384
VCGCHYWQGGGHHHPQHHKTDVPVQDRRA*EGERRCS*KSHQCALHP
Sbjct: 920 VCGCHYWQGGGHHHPQHHKTDVPVQDRRA*EGERRCS*KSHQCALHP 1054

Score = 117 bits (251), Expect(6) = 0.0
Identities = 52/55 (94%), Positives = 52/55 (94%)
Frame = -3 / -2

Query: 1703 KPEGNFIFLPTEV*STLLVGPCELL*TIHV*KCLALXFLTTPRGAXSVGPIGWVFG 1539
KPEGNFIFLPTEV*STLLVGPCELL*TIHV*KCLAL FLTTPRGA SVGPIG VFG
Sbjct: 2380 KPEGNFIFLPTEV*STLLVGPCELL*TIHV*KCLALEFLTTPRGADSVGPIG*VFG 2216

Score = 111 bits (238), Expect(5) = 0.0
Identities = 44/46 (95%), Positives = 44/46 (95%)
Frame = -1 / -3

Query: 1702 NLKEILFFFPLRCDPPSWWGLESFFKQSTFKSALRXNF*HPEGXTV 1565
NLKEILFFFPLRCDPPSWWGLESFFKQSTFKSALR NF*HPEG TV
Sbjct: 2379 NLKEILFFFPLRCDPPSWWGLESFFKQSTFKSALR*NF*HPEGQTV 2242

Score = 85.4 bits (180), Expect(5) = 0.0
Identities = 31/31 (100%), Positives = 31/31 (100%)
Frame = -2 / -2

Query: 129 FSGPCAICSSGM*ETFRAWFSNWWPFSFMA 37
FSGPCAICSSGM*ETFRAWFSNWWPFSFMA
Sbjct: 799 FSGPCAICSSGM*ETFRAWFSNWWPFSFMA 707

Score = 83.1 bits (175), Expect(5) = 0.0
Identities = 35/36 (97%), Positives = 35/36 (97%)
Frame = -1 / -1

Query: 820 AIGSSPSNAAGRRRDCAG*SWEKTYSSQVQARDQVR 713
AIGSSPSNAAGRRRDCAG*SWEKTYSSQVQAR QVR
Sbjct: 1496 AIGSSPSNAAGRRRDCAG*SWEKTYSSQVQARGQVR 1389

Score = 81.2 bits (171), Expect(6) = 0.0
Identities = 35/49 (71%), Positives = 35/49 (71%)
Frame = -3 / -3

Query: 182 QVSPGGADPESQSPLGAHSQVPVLSAHRGCRRXXXXXXXXXXXXXXXXXX*WL 36
QVSPGGADPESQSPLGAHSQVPVLSAHRGCRR *WL
Sbjct: 852 QVSPGGADPESQSPLGAHSQVPVLSAHRGCRRPSGHGSPTGGHSAS*WL 706

Score = 56.5 bits (117), Expect(6) = 0.0
Identities = 21/21 (100%), Positives = 21/21 (100%)
Frame = -3 / -3

Query: 809 QPQ*RCWEAAGLRWMKLGKDL 747
QPQ*RCWEAAGLRWMKLGKDL
Sbjct: 1485 QPQ*RCWEAAGLRWMKLGKDL 1423

Score = 42.8 bits (87), Expect(3) = 4e-38
Identities = 13/37 (35%), Positives = 26/37 (70%)
Frame = +2 / +3

Query: 461 EVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITI 571
++PL++L +VG +IGKEG ++ + + T++KI +
Sbjct: 888 DIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDV 998

Score = 41.4 bits (84), Expect(2) = 6e-06
Identities = 13/37 (35%), Positives = 25/37 (67%)
Frame = +2 / +3

Query: 218 DIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDV 328
++PL+ L +VG +IGKEG ++ + + T++KI +
Sbjct: 1131 EVPLKTLAHNNFVGRLIGKEGRNLKKVEQDTETKITI 1241

Score = 40.9 bits (83), Expect(3) = 4e-38
Identities = 13/44 (29%), Positives = 26/44 (59%)
Frame = +2 / +3

Query: 863 IPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVI 994
+PA A G +IGK G+ + +L +A + + +TPD ++++
Sbjct: 1785 VPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIV 1916

Score = 40.9 bits (83), Expect(2) = 6e-06
Identities = 13/44 (29%), Positives = 26/44 (59%)
Frame = +2 / +3

Query: 1109 VPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIV 1240
+PA A G +IGK G+ + +L +A + + +TPD ++++
Sbjct: 1539 IPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVI 1670

Score = 38.6 bits (78), Expect = 6.8
Identities = 15/54 (27%), Positives = 30/54 (55%)
Frame = +2 / +3

Query: 851 VQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPE 1012
+++ +P Q VGAIIGK+G I+ +++ + I + E + + + + PE
Sbjct: 897 LRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPE 1058

Score = 38.6 bits (78), Expect = 6.8
Identities = 15/54 (27%), Positives = 30/54 (55%)
Frame = +2 / +3

Query: 227 LRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPE 388
 +++ +P Q VGAIIGK+G I+ +++ + I + E + + + + PE
 Sbjct: 1527 VQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPE 1688

Score = 35.4 bits (71), Expect(6) = 0.0
 Identities = 11/11 (100%), Positives = 11/11 (100%)
 Frame = -3 / -3

Query: 260 HPHTGWAPGAE 228
 HPHTGWAPGAE
 Sbjct: 930 HPHTGWAPGAE 898

Score = 30.4 bits (60), Expect(5) = 0.0
 Identities = 12/13 (92%), Positives = 13/13 (100%)
 Frame = +3 / +1

Query: 30 PGEPS*S*MATSW 68
 PG+PS*S*MATSW
 Sbjct: 700 PGKPS*S*MATSW 738

Score = 26.7 bits (52), Expect(6) = 0.0
 Identities = 11/11 (100%), Positives = 11/11 (100%)
 Frame = +3 / +1

Query: 747 *VFSQLHPAQS 779
 *VFSQLHPAQS
 Sbjct: 1423 *VFSQLHPAQS 1455

>gi|7141071|gb|AF198254.1|AF198254 Homo sapiens mRNA-binding protein CRDBP m
 Length = 2381

Score = 576 bits (1252), Expect(3) = 0.0
 Identities = 251/279 (89%), Positives = 253/279 (90%)
 Frame = +2 / +3

Query: 704 AMSSHLIPGLNLAAGVLFXXXXXXXXXXXXXXXXXTGAAPYSSFMQAPEQEMVQVFIPAQAVG 883
 ++ SHL PGLNLAAGVLF TGAAPYSSFMQAPEQEMVQVFIPAQAVG
 Sbjct: 1380 SLQSHLTPGLNLAAGVLFPASSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVG 1559

Query: 884 AIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEEN 1063
 AIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEEN
 Sbjct: 1560 AIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEEN 1739

Query: 1064 FFGPKKEEVKLETHIRVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVK 1243
 FFGPKKEEVKLETHIRVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVK
 Sbjct: 1740 FFGPKKEEVKLETHIRVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVK 1919

Query: 1244 IIGHFYASQMAQRKIRDILAQVKQHQKQGSNQAQARRKXXXXXXXXXESRTTGRNRECA 1423
 IIGHFYASQMAQRKIRDILAQVKQHQKQGSNQAQARRK ESRTTGRNRECA
 Sbjct: 1920 IIGHFYASQMAQRKIRDILAQVKQHQKQGSNQAQARRK*PAPPCPFESRTTGRNRECA 2099

Query: 1424 LPGRPENEWESGTXGPGCRSGLPT*LRKMFQ*GTLIXQP 1540

LPGRPENEWESGT GPGCRSGLPT*LRKMFQ*GTLI QP
 Sbjct: 2100 LPGRPENEWESGTPGPGCRSGLPT*LRKMFQ*GTLI SQP 2216

Score = 555 bits (1206), Expect(4) = 0.0
 Identities = 227/237 (95%), Positives = 232/237 (97%)
 Frame = -1 / -1

Query: 739 QVQARDQVRAHGSHIILIGLPNLFHYFLLGPATILDGPLHSDGPLRVVKGKVLQRGDGDF 560
 Q + + +++AHGSHIILIGLPNLFHYFLLGPATILDGPLHSDGPLRVVKGKVLQRGDGDF
 Sbjct: 1409 QARGQVRLQAHGSHIILIGLPNLFHYFLLGPATILDGPLHSDGPLRVVKGKVLQRGDGDF 1230

Query: 559 CLGILLYLLQVPSFLANETPYKVIMGQDLQGNLVSFRFVLSLFMHNLDHLTSGGAALRG 380
 CLGILLYLLQVPSFLANETPYKVIMGQ LQGNLVSFRFVLSLFMHNLDHLTSGGAALRG
 Sbjct: 1229 CLGILLYLLQVPSFLANETPYKVIMGQGLQGNLVSFRFVLSLFMHNLDHLTSGGAALRG 1050

Query: 379 GVHTDGGFFSCTCVLLPMHVYLGLGLFCDVADGGPLLANNNGTHILGGHQEPKGDVHLLLLG 200
 GVHTDGGFFSCTCVLLPMHVYLGLGLFCDVADGGPLLANNNGTHILGGHQEPKGDVHLLLLG
 Sbjct: 1049 GVHTDGGFFSCTCVLLPMHVYLGLGLFCDVADGGPLLANNNGTHILGGHQEPKGDVHLLLLG 870

Query: 199 WGPRCHR*ALAGLTPRAKAPSAPILRSLCYLLIGDVGDLQGMVLQLVAIQLHDGSPG 29
 WGPRCHR*ALAGLTPRAKAPSAPILRSLCYLLIGDVGDLQGMVLQLVAIQLHDG PG
 Sbjct: 869 WGPRCHR*ALAGLTPRAKAPSAPILRSLCYLLIGDVGDLQGMVLQLVAIQLHDGLPG 699

Score = 527 bits (1145), Expect(3) = 0.0
 Identities = 225/227 (99%), Positives = 225/227 (99%)
 Frame = +2 / +3

Query: 32 RGAIMKLNGHQLENHALKVSYPDEQIAQGPENRRGGFGSRGQPRQGS PVAAGAPAKQQ 211
 R AIMKLNGHQLENHALKVSYPDEQIAQGPENRRGGFGSRGQPRQGS PVAAGAPAKQQ
 Sbjct: 702 RGAIMKLNGHQLENHALKVSYPDEQIAQGPENRRGGFGSRGQPRQGS PVAAGAPAKQQ 881

Query: 212 QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 391
 QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG
 Sbjct: 882 QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 1061

Query: 392 CSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLLIGKEGRNLKKVEQDTETKITI 571
 CSSACKMILEIMHKEAKDTKTADDEVPLK LAHNNFVGRLLIGKEGRNLKKVEQDTETKITI
 Sbjct: 1062 CSSACKMILEIMHKEAKDTKTADDEVPLKTLAHNNFVGRLLIGKEGRNLKKVEQDTETKITI 1241

Query: 572 SSLQDLTLYNPRTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS 712
 SSLQDLTLYNPRTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS
 Sbjct: 1242 SSLQDLTLYNPRTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS 1382

Score = 522 bits (1133), Expect(5) = 0.0
 Identities = 218/242 (90%), Positives = 220/242 (90%)
 Frame = -3 / -3

Query: 1583 PRGAXSVGPVGWVFGAXRSGFLTGTSTFSIKWANLIYSPA XVSRIPTH SQACRGEHTLDFC 1404
 P G +G +G GA RSGFLTGTSTFSIKWANLIYSPA XVSRIPTH SQACRGEHTLDFC
 Sbjct: 2259 PEGQTVLQGLGRCLGAERSGFLTGTSTFSIKWANLIYSPA QVSRIPTH SQACRGEHTLDFC 2080

Query: 1403 PLLSWTXRDREGLVTXXXXXXXXXXXXSDAAA*PGPGCLGSSVEPSDWHNRNVR*FSR*PGR 1224

PLLSWT RDREGLVT SDAAA*PGPGCLGSSVEPSDWHRNVR*FSR*PGR
Sbjct: 2079 PLLSWTRRDREGLVTSFVPGPGYSVPSDAAA*PGPGCLGSSVEPSDWHRNVR*FSR*PGR 1900

Query: 1223 SHQGSGLLVLPQLPSNSATRSPPFFHLCQ*PGQLMLAHVCGSPASLPPWDQRSSPP*VC 1044
SHQGSGLLVLPQLPSNSATRSPPFFHLCQ*PGQLMLAHVCGSPASLPPWDQRSSPP*VC
Sbjct: 1899 SHQGSGLLVLPQLPSNSATRSPPFFHLCQ*PGQLMLAHVCGSPASLPPWDQRSSPP*VC 1720

Query: 1043 HRFFPEP*IGPLAVQ***PYELWSQVFRVVQS*WRRWQTGRAV*CAAPSCR*WRPLPGRG 864
HRFFPEP*IGPLAVQ***PYELWSQVFRVVQS*WRRWQTGRAV*CAAPSCR*WRPLPGRG
Sbjct: 1719 HRFFPEP*IGPLAVQ***PYELWSQVFRVVQS*WRRWQTGRAV*CAAPSCR*WRPLPGRG 1540

Query: 863 *T 858
*T
Sbjct: 1539 *T 1534

Score = 510 bits (1108), Expect(6) = 0.0
Identities = 210/225 (93%), Positives = 210/225 (93%)
Frame = +3 / +1

Query: 837 PSRRWCRCCLSPPRQWAPXXXXXXXXXXXXXPGLPAPPSRLHHPKHLTPKFVWLSSLDRQRP 1016
PSRRWCRCCLSPPRQWAP PGLPAPPSRLHHPKHLTPKFVWLSSLDRQRP
Sbjct: 1513 PSRRWCRCCLSPPRQWAPSSARRGSTSNSSPGLPAPPSRLHHPKHLTPKFVWLSSLDRQRP 1692

Query: 1017 NSRLREESMANSRRRTSLVPRRK*SWRPTYVCQHQQLAGSLAKVEKR*TSCRI*RQLRW* 1196
NSRLREESMANSRRRTSLVPRRK*SWRPTYVCQHQQLAGSLAKVEKR*TSCRI*RQLRW*
Sbjct: 1693 NSRLREESMANSRRRTSLVPRRK*SWRPTYVCQHQQLAGSLAKVEKR*TSCRI*RQLRW* 1872

Query: 1197 YQETRPLMRTTRSS*KSSDISMPVRWLNGRSETSWPRLSSSIRRDRVTRPRHGGSDQPLP 1376
YQETRPLMRTTRSS*KSSDISMPVRWLNGRSETSWPRLSSSIRRDRVTRPRH GSDQPLP
Sbjct: 1873 YQETRPLMRTTRSS*KSSDISMPVRWLNGRSETSWPRLSSSIRRDRVTRPRHEGSDQPLP 2052

Query: 1377 VPXSPGQQRAEIESVLSPAGLRMSGNPGHXGRAVDQVCPLD*ERC 1511
VP SPGQQRAEIESVLSPAGLRMSGNPGH GRAVDQVCPLD*ERC
Sbjct: 2053 VPSSPGQQRAEIESVLSPAGLRMSGNPGHLGRAVDQVCPLD*ERC 2187

Score = 504 bits (1094), Expect(5) = 0.0
Identities = 194/194 (100%), Positives = 194/194 (100%)
Frame = +1 / +2

Query: 715 SPDPWPEPGCCRSFPSFIQRSPAASQQRYWGCSL*LLYAGSRAGDGAGVYPRPGSGRHHR 894
SPDPWPEPGCCRSFPSFIQRSPAASQQRYWGCSL*LLYAGSRAGDGAGVYPRPGSGRHHR
Sbjct: 1391 SPDPWPEPGCCRSFPSFIQRSPAASQQRYWGCSL*LLYAGSRAGDGAGVYPRPGSGRHHR 1570

Query: 895 QEGAAHQ TALPVCQRLHQDCTTRNT*LQSSYGYHHWTARGPIQGSGKNLWQTQGGELLWS 1074
QEGAAHQ TALPVCQRLHQDCTTRNT*LQSSYGYHHWTARGPIQGSGKNLWQTQGGELLWS
Sbjct: 1571 QEGAAHQ TALPVCQRLHQDCTTRNT*LQSSYGYHHWTARGPIQGSGKNLWQTQGGELLWS 1750

Query: 1075 QGGSEAGDPHTCASISSWPGHQWRWKNGERVAEFDGS*GGSTKRDPD**ERPGHRENHRT 1254
QGGSEAGDPHTCASISSWPGHQWRWKNGERVAEFDGS*GGSTKRDPD**ERPGHRENHRT
Sbjct: 1751 QGGSEAGDPHTCASISSWPGHQWRWKNGERVAEFDGS*GGSTKRDPD**ERPGHRENHRT 1930

Query: 1255 FLCQSDGSTEDPRH 1296

FLCQSDGSTEDPRH

Sbjct: 1931 FLCQSDGSTEDPRH 1972

Score = 482 bits (1046), Expect(6) = 0.0
 Identities = 196/213 (92%), Positives = 196/213 (92%)
 Frame = -1 / -1

Query: 1513 EHLSQSSGQT*STARPCPGFPLILRPAGESTLSISARCCPGLXGTGRGWSLPPCXXXXX 1334
 EHLSQSSGQT*STARPCPGFPLILRPAGESTLSISARCCPGL GTGRGWSLP C
 Sbjct: 2189 EHLSQSSGQT*STARPCPGFPLILRPAGESTLSISARCCPGLXGTGRGWSLPPCGLGLVT 2010

Query: 1333 XXXXXXXXXXXLGQDVSDLPLSHLTGIEMSDDFHDDLVLIRGLVSWYHLSRQILQLVHR 1154
 LGQDVSDLPLSHLTGIEMSDDFHDDLVLIRGLVSWYHLSRQILQLVHR
 Sbjct: 2009 LSLMLLLNLGQDVSDLPLSHLTGIEMSDDFHDDLVLIRGLVSWYHLSRQILQLVHR 1830

Query: 1153 FSTFANDPASC*CWHTYVGLQLHFLLGTKEVLLLEFAIDSSLSLELGLWRSSDDNHTNFG 974
 FSTFANDPASC*CWHTYVGLQLHFLLGTKEVLLLEFAIDSSLSLELGLWRSSDDNHTNFG
 Sbjct: 1829 FSTFANDPASC*CWHTYVGLQLHFLLGTKEVLLLEFAIDSSLSLELGLWRSSDDNHTNFG 1650

Query: 973 VRCFGWCNLDGGAGKPGELFDVLP LLADDGAHC 875
 VRCFGWCNLDGGAGKPGELFDVLP LLADDGAHC
 Sbjct: 1649 VRCFGWCNLDGGAGKPGELFDVLP LLADDGAHC 1551

Score = 395 bits (857), Expect(5) = 0.0
 Identities = 168/179 (93%), Positives = 169/179 (94%)
 Frame = -2 / -2

Query: 711 LMAATSFS*ASRTFFIISCSALQQFSMAPFTVMVLSGL*RVRSCNEEMVIFVSVSCSTFF 532
 LMAATSFS*ASRTFFIISCSALQQFSMAPFTVMVLSGL*RVRSCNEEMVIFVSVSCSTFF
 Sbjct: 1381 LMAATSFS*ASRTFFIISCSALQQFSMAPFTVMVLSGL*RVRSCNEEMVIFVSVSCSTFF 1202

Query: 531 RFRPSLPMRRPTKLLWARIFRGTXXXXXXXXXXXLCIISKIILQAEQPSGVECTLMAFSA 352
 RFRPSLPMRRPTKLLWAR+FRGT LCIISKIILQAEQPSGVECTLMAFSA
 Sbjct: 1201 RFRPSLPMRRPTKLLWARVFRGTSSAVLVSLASLCIISKIILQAEQPSGVECTLMAFSA 1022

Query: 351 APAFSFLCTSILDWVCFVMLRMVAPSLPIMAPTYWVGTRSRRMSTCCCLAGAPAATGE 175
 APAFSFLCTSILDWVCFVMLRMVAPSLPIMAPTYWVGTRSRRMSTCCCLAGAPAATGE
 Sbjct: 1021 APAFSFLCTSILDWVCFVMLRMVAPSLPIMAPTYWVGTRSRRMSTCCCLAGAPAATGE 845

Score = 374 bits (810), Expect(4) = 0.0
 Identities = 150/152 (98%), Positives = 150/152 (98%)
 Frame = -2 / -2

Query: 1539 G*XIRVPHWNIFLNQVGKPDLPQGPXVPDSSHFSGLPGRAHSRFLPVVVLD SKGQGGAGH 1360
 G* IRVPHWNIFLNQVGKPDLPQGP VPDSSHFSGLPGRAHSRFLPVVVLD SKGQGGAGH
 Sbjct: 2215 G*EIRVPHWNIFLNQVGKPDLPQGPVDPDSSHFSGLPGRAHSRFLPVVVLD SKGQGGAGH 2036

Query: 1359 FLRAWAWLLCPF*CCCLTWARMSRIFR*AI*LA*KCPMIFTMTWSFSSGVWSLGTTSAA 1180
 FLRAWAWLLCPF*CCCLTWARMSRIFR*AI*LA*KCPMIFTMTWSFSSGVWSLGTTSAA
 Sbjct: 2035 FLRAWAWLLCPF*CCCLTWARMSRIFR*AI*LA*KCPMIFTMTWSFSSGVWSLGTTSAA 1856

Query: 1179 VKFCNSFTVFPPLPMTRPAADAGTRMWSSFT 1084

VKFCNSFTVFPPLPMTRPAADAGTRMWSSFT
Sbjct: 1855 VKFCNSFTVFPPLPMTRPAADAGTRMWSSFT 1760

Score = 269 bits (582), Expect(6) = 0.0
Identities = 113/134 (84%), Positives = 113/134 (84%)
Frame = -3 / -3

Query: 701 PHHSHRPPELSSLFPARPCNNSRXXXXXXXXXXQGCKG*GLATRRW*FLSRYLALPSSGSV 522
PHHSHRPPELSSLFPARPCNNSR QGCKG*GLATRRW*FLSRYLALPSSGSV
Sbjct: 1371 PHHSHRPPELSSLFPARPCNNSRWPPSQ*WSSQGCKG*GLATRRW*FLSRYLALPSSGSV 1192

Query: 521 LPCQ*DALQSYYPGSSGEPRQPFWCP*PLYAXXXXXXXXXXXXXPQGWSAH*WLFQLHLR 342
LPCQ*DALQSYYPGSSGEPRQPFWCP*PLYA PQGWSAH*WLFQLHLR
Sbjct: 1191 LPCQ*DALQSYYPGSSGEPRQPFWCP*PLYA*SPRSSYKRRSSPQGWSAH*WLFQLHLR 1012

Query: 341 SPSYARLSWTGSVL 300
SPSYARLSWTGSVL
Sbjct: 1011 SPSYARLSWTGSVL 970

Score = 247 bits (534), Expect(4) = 0.0
Identities = 101/103 (98%), Positives = 103/103 (100%)
Frame = -2 / -2

Query: 1020 NWASGGPVMITIRTLESQVSGGAILMEALANRESCLMCCPFLPMMAPTAWAGINTCTISC 841
NWASGGPVMITIRTLESQVSGGAILMEALANRESCLMCCPFLPMMAPTAWAGINTCTISC
Sbjct: 1696 NWASGGPVMITIRTLESQVSGGAILMEALANRESCLMCCPFLPMMAPTAWAGINTCTISC 1517

Query: 840 SGACIKEL*GAAPVTLLGGGGTALDEAGKRPTAARFRPGIR*E 712
SGACIKEL*GAAPVTLLGGGGTALDEAGKRPTAARFRPG+R*+
Sbjct: 1516 SGACIKEL*GAAPVTLLGGGGTALDEAGKRPTAARFRPGVR*D 1388

Score = 227 bits (491), Expect(6) = 0.0
Identities = 98/99 (98%), Positives = 98/99 (98%)
Frame = +3 / +1

Query: 414 SWRLCIKRLRTPKRLTRFP*RSWPIITL*GVSLARKDGT*RR*SKIPRQKSPSPRCKTLP 593
SWRLCIKRLRTPKRLTRFP*R WPIITL*GVSLARKDGT*RR*SKIPRQKSPSPRCKTLP
Sbjct: 1084 SWRLCIKRLRTPKRLTRFP*RPWPIITL*GVSLARKDGT*RR*SKIPRQKSPSPRCKTLP 1263

Query: 594 FTTLRGPSL*RGPSRIVAGPSRK**RKFGRPMMRWLP* 710
FTTLRGPSL*RGPSRIVAGPSRK**RKFGRPMMRWLP*
Sbjct: 1264 FTTLRGPSL*RGPSRIVAGPSRK**RKFGRPMMRWLP* 1380

Score = 223 bits (482), Expect(5) = 0.0
Identities = 88/88 (100%), Positives = 88/88 (100%)
Frame = +3 / +1

Query: 114 HRDLRMGAEGALALGVSPARHLWQRGQPSSSKWTSPFGSWCPSMWWPLLARRGPPSA 293
HRDLRMGAEGALALGVSPARHLWQRGQPSSSKWTSPFGSWCPSMWWPLLARRGPPSA
Sbjct: 784 HRDLRMGAEGALALGVSPARHLWQRGQPSSSKWTSPFGSWCPSMWWPLLARRGPPSA 963

Query: 294 TSQNRPSR*TCIGRRTQVQLKKPSVCT 377

TSQNRPSPR*TCIGRRTQVQLKKPSVCT
Sbjct: 964 TSQNRPSPR*TCIGRRTQVQLKKPSVCT 1047

Score = 196 bits (422), Expect(5) = 0.0
Identities = 78/78 (100%), Positives = 78/78 (100%)
Frame = +1 / +2

Query: 424 YA*RG*GHQNG*RGSPEDPGP**LCRASHWQGRTEPEEGRARYRDKNHLLVARPYPLQP 603
YA*RG*GHQNG*RGSPEDPGP**LCRASHWQGRTEPEEGRARYRDKNHLLVARPYPLQP
Sbjct: 1094 YA*RG*GHQNG*RGSPEDPGP**LCRASHWQGRTEPEEGRARYRDKNHLLVARPYPLQP 1273

Query: 604 *EDHHCEGGHRELLQGRA 657
*EDHHCEGGHRELLQGRA
Sbjct: 1274 *EDHHCEGGHRELLQGRA 1327

Score = 141 bits (303), Expect(4) = 0.0
Identities = 54/56 (96%), Positives = 54/56 (96%)
Frame = -2 / -1

Query: 1704 KT*RKFYFSSH*GVIHPLGGAWRASLNNPRLKVPCAXISDTPRGXQCWANWVGWVG 1537
KT*RKFYFSSH*GVIHPLGGAWRASLNNPRLKVPCA ISDTPRG QCWANWVGWVG
Sbjct: 2381 KT*RKFYFSSH*GVIHPLGGAWRASLNNPRLKVPCARISDTPRGRQCWANWVGWVG 2214

Score = 136 bits (291), Expect(5) = 0.0
Identities = 60/71 (84%), Positives = 60/71 (84%)
Frame = +1 / +2

Query: 1372 SLSLXVQDNNGQKSRVCSPRQA*E*VGIRDTWAGL*IRFAHLIEKDVPVRNPDLAPNTH 1551
SLSL VQDNNGQKSRVCSPRQA*E*VGIRDTWAGL*IRFAHLIEKDVPVRNPDLAP
Sbjct: 2048 SLSLRVQDNNGQKSRVCSPRQA*E*VGIRDTWAGL*IRFAHLIEKDVPVRNPDLAPKHL 2227

Query: 1552 PIGPTLXAPRG 1584
P P P G
Sbjct: 2228 PNWPNTVCPSPG 2260

Score = 133 bits (284), Expect(3) = 0.0
Identities = 53/55 (96%), Positives = 53/55 (96%)
Frame = +2 / +1

Query: 1538 PQTPTQLAQHCXPLGVSEIXAQGTFRGLFKEALQAPPRGWITPQWEEK*NFLQV 1702
PQTPTQLAQHC PLGVSEI AQGTFRGLFKEALQAPPRGWITPQWEEK*NFLQV
Sbjct: 2215 PQTPTQLAQHCLPLGVSEILAQGTFRGLFKEALQAPPRGWITPQWEEK*NFLQV 2379

Score = 133 bits (284), Expect(6) = 0.0
Identities = 52/54 (96%), Positives = 52/54 (96%)
Frame = +3 / +2

Query: 1542 KHPPNWPNTVCPSPGCQKX*RKALLNVDCLKKLSRPHQEGGSHLSGKKNKISFRF 1703
KH PNWPNTVCPSPGCQK *RKALLNVDCLKKLSRPHQEGGSHLSGKKNKISFRF
Sbjct: 2219 KHLPNWPNTVCPSPGCQKF*RKALLNVDCLKKLSRPHQEGGSHLSGKKNKISFRF 2380

Score = 132 bits (282), Expect(6) = 0.0

Identities = 50/55 (90%), Positives = 50/55 (90%)
Frame = +1 / +2

Query: 19 PQFTPGSHHEAWPPVGEPCEGLLHPR*ADSTGT*EWAPRGLWLSGSAPPGLTC 183
P SHHEAEWPPVGEPCEGLLHPR*ADSTGT*EWAPRGLWLSGSAPPGLTC
Sbjct: 689 PGADQASHHEAEWPPVGEPCEGLLHPR*ADSTGT*EWAPRGLWLSGSAPPGLTC 853

Score = 129 bits (276), Expect(3) = 4e-38
Identities = 52/55 (94%), Positives = 53/55 (96%)
Frame = +1 / +3

Query: 1540 PNTHPIGPTLXAPRGVRNXSARHF*TWIV*RSSPGPTKRVDHTSVGRKIKFPSGF 1704
PNT+PIGPTL APRGVRN SARHF*TWIV*RSSPGPTKRVDHTSVGRKIKFPSGF
Sbjct: 2217 PNTYPIGPTLSAPRGVRNSSARHF*TWIV*RSSPGPTKRVDHTSVGRKIKFPSGF 2381

Score = 125 bits (268), Expect(6) = 0.0
Identities = 45/45 (100%), Positives = 45/45 (100%)
Frame = +1 / +2

Query: 250 VCGCHYWQGGGHHHPQHHKTDVPVQDRRA*EGERRCS*KSHQCALHP 384
VCGCHYWQGGGHHHPQHHKTDVPVQDRRA*EGERRCS*KSHQCALHP
Sbjct: 920 VCGCHYWQGGGHHHPQHHKTDVPVQDRRA*EGERRCS*KSHQCALHP 1054

Score = 117 bits (251), Expect(6) = 0.0
Identities = 52/55 (94%), Positives = 52/55 (94%)
Frame = -3 / -2

Query: 1703 KPEGNFIFLPTEV*STLLVGPCELL*TIHV*KCLALXFLTPRGAXSVGPIGWVFG 1539
KPEGNFIFLPTEV*STLLVGPCELL*TIHV*KCLAL FLTPRGA SVGPIG VFG
Sbjct: 2380 KPEGNFIFLPTEV*STLLVGPCELL*TIHV*KCLALEFLTPRGADSVGPIG*VFG 2216

Score = 111 bits (238), Expect(5) = 0.0
Identities = 44/46 (95%), Positives = 44/46 (95%)
Frame = -1 / -3

Query: 1702 NLKEILFFFPLRCDPPSWWGLESFFKQSTFKSALRXNF*HPEGXTV 1565
NLKEILFFFPLRCDPPSWWGLESFFKQSTFKSALR NF*HPEG TV
Sbjct: 2379 NLKEILFFFPLRCDPPSWWGLESFFKQSTFKSALR*NF*HPEGQTV 2242

Score = 85.4 bits (180), Expect(5) = 0.0
Identities = 31/31 (100%), Positives = 31/31 (100%)
Frame = -2 / -2

Query: 129 FSGPCAICSSGM*ETFRAWFSNWWPFSFMMA 37
FSGPCAICSSGM*ETFRAWFSNWWPFSFMMA
Sbjct: 799 FSGPCAICSSGM*ETFRAWFSNWWPFSFMMA 707

Score = 83.1 bits (175), Expect(5) = 0.0
Identities = 35/36 (97%), Positives = 35/36 (97%)
Frame = -1 / -1

Query: 820 AIGSSPSNAAGRRRDCAG*SWEKTYSSQVQARDQVR 713

AIGSSPSNAAGRRRDCAG*SWEKTYSSQVQAR QVR
Sbjct: 1496 AIGSSPSNAAGRRRDCAG*SWEKTYSSQVQARGQVR 1389

Score = 81.2 bits (171), Expect(6) = 0.0
Identities = 35/49 (71%), Positives = 35/49 (71%)
Frame = -3 / -3

Query: 182 QVSPGGADPESQSPLGAHSQVPVLSAHRGCRRXXXXXXXXXXXXXXXXXX*WL 36
QVSPGGADPESQSPLGAHSQVPVLSAHRGCRR *WL
Sbjct: 852 QVSPGGADPESQSPLGAHSQVPVLSAHRGCRRPSGHGSPTGGHSAS*WL 706

Score = 56.5 bits (117), Expect(6) = 0.0
Identities = 21/21 (100%), Positives = 21/21 (100%)
Frame = -3 / -3

Query: 809 QPQ*RCWEAAGLRWMKLGKDL 747
QPQ*RCWEAAGLRWMKLGKDL
Sbjct: 1485 QPQ*RCWEAAGLRWMKLGKDL 1423

Score = 42.8 bits (87), Expect(3) = 4e-38
Identities = 13/37 (35%), Positives = 26/37 (70%)
Frame = +2 / +3

Query: 461 EVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITI 571
++PL++L +VG +IGKEG ++ + + T++KI +
Sbjct: 888 DIPLRLLVPTQYVGAIIIGKEGATIRNITKQTQSKIDV 998

Score = 41.4 bits (84), Expect(2) = 6e-06
Identities = 13/37 (35%), Positives = 25/37 (67%)
Frame = +2 / +3

Query: 218 DIPLRLLVPTQYVGAIIIGKEGATIRNITKQTQSKIDV 328
++PL+ L +VG +IGKEG ++ + + T++KI +
Sbjct: 1131 EVPLKTLAHNNFVGRLIGKEGRNLKKVEQDTETKITI 1241

Score = 40.9 bits (83), Expect(3) = 4e-38
Identities = 13/44 (29%), Positives = 26/44 (59%)
Frame = +2 / +3

Query: 863 IPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVI 994
+PA A G +IGK G+ + +L +A + + +TPD ++++
Sbjct: 1785 VPASAAGRVIGKGKGTVNELQNLTAAEVVVPRDQTPDENDQVIV 1916

Score = 40.9 bits (83), Expect(2) = 6e-06
Identities = 13/44 (29%), Positives = 26/44 (59%)
Frame = +2 / +3

Query: 1109 VPASAAGRVIGKGKGTVNELQNLTAAEVVVPRDQTPDENDQVIV 1240
+PA A G +IGK G+ + +L +A + + +TPD ++++
Sbjct: 1539 IPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVI 1670

Score = 38.6 bits (78), Expect = 6.8

Identities = 15/54 (27%), Positives = 30/54 (55%)
 Frame = +2 / +3

Query: 851 VQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPE 1012
 +++ +P Q VGAIIGK+G I+ +++ + I + E + + + + PE
 Sbjct: 897 LRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPE 1058

Score = 38.6 bits (78), Expect = 6.8
 Identities = 15/54 (27%), Positives = 30/54 (55%)
 Frame = +2 / +3

Query: 227 LRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPE 388
 +++ +P Q VGAIIGK+G I+ +++ + I + E + + + + PE
 Sbjct: 1527 VQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPE 1688

Score = 35.4 bits (71), Expect(6) = 0.0
 Identities = 11/11 (100%), Positives = 11/11 (100%)
 Frame = -3 / -3

Query: 260 HPHTGWAPGAE 228
 HPHTGWAPGAE
 Sbjct: 930 HPHTGWAPGAE 898

Score = 30.4 bits (60), Expect(5) = 0.0
 Identities = 12/13 (92%), Positives = 13/13 (100%)
 Frame = +3 / +1

Query: 30 PGEPS*S*MATSW 68
 PG+PS*S*MATSW
 Sbjct: 700 PGKPS*S*MATSW 738

Score = 26.7 bits (52), Expect(6) = 0.0
 Identities = 11/11 (100%), Positives = 11/11 (100%)
 Frame = +3 / +1

Query: 747 *VFSQLHPAQS 779
 *VFSQLHPAQS
 Sbjct: 1423 *VFSQLHPAQS 1455

>gi|24580458|gb|AC105030.11| **D** Homo sapiens chromosome 17, clone CTD-2244F11, comp
 Length = 107848

Score = 363 bits (786), Expect(10) = 0.0
 Identities = 142/146 (97%), Positives = 142/146 (97%)
 Frame = -2 / +2

Query: 1707 FKT*RKIFYSSH*GVIHPLGGAWRASLNNPRLKVPCAXISDTPRGXQCWANWVGWVG*XI 1528
 FKT*RKIFYSSH*GVIHPLGGAWRASLNNPRLKVPCA ISDTPRG QCWANWVGWVG* I
 Sbjct: 72236 FKT*RKIFYSSH*GVIHPLGGAWRASLNNPRLKVPCARISDTPRGRQCWANWVGWVG*EI 72415

Query: 1527 RVPHWNIFLNQVGKPDLPQGPXVPDSHSFSGLPGRAHSRFLPVVVLDKSGQGGAGHFLRA 1348
 RVPHWNIFLNQVGKPDLPQGP VPDSHSFSGLPGRAHSRFLPVVVLDKSGQGGAGHFLRA
 Sbjct: 72416 RVPHWNIFLNQVGKPDLPQGPVPDSHSFSGLPGRAHSRFLPVVVLDKSGQGGAGHFLRA 72595

Query: 1347 WAWLLCPF*CCCLTWARMSRIFR*AI 1270
WAWLLCPF*CCCLTWARMSRIFR*AI
Sbjct: 72596 WAWLLCPF*CCCLTWARMSRIFR*AI 72673

Score = 326 bits (706), Expect(10) = 0.0
Identities = 133/146 (91%), Positives = 133/146 (91%)
Frame = +3 / -3

Query: 1269 RWLNGRSETSWPRLSSSIRRDVTRPRHGGSDQPLPVPXSPGQQRAEIESVLSPAGLRMS 1448
RWLNGRSETSWPRLSSSIRRDVTRPRHGGSDQPLPVP SPGQQRAEIESVLSPAGLRMS
Sbjct: 72674 RWLNGRSETSWPRLSSSIRRDVTRPRHGGSDQPLPVPSSPGQQRAEIESVLSPAGLRMS 72495

Query: 1449 GNPBGHXGRAVDQVCPLD*ERCXXXXXXXXXXKHPPNWPNTVCPSGCQKX*RKALLNVDCL 1628
GNPBGH GRAVDQVCPLD*ERC KHPPNWPNTVCPSGCQK *RKALLNVDCL
Sbjct: 72494 GNPBGHLGRAVDQVCPLD*ERCSSEEP*SLSPKHPPNWPNTVCPSGCQKF*RKALLNVDCL 72315

Query: 1629 KKLSRPHQEGGSHLSGKKNKISFRF* 1706
KKLSRPHQEGGSHLSGKKNKISFRF*
Sbjct: 72314 KKLSRPHQEGGSHLSGKKNKISFRF* 72237

Score = 318 bits (688), Expect(12) = 0.0
Identities = 135/147 (91%), Positives = 135/147 (91%)
Frame = +2 / -2

Query: 1268 QMAQRKIRDILAQVKQHQKQSNQAQARRXXXXXXXXXESRTTGRNRECALPGRPENE 1447
QMAQRKIRDILAQVKQHQKQSNQAQARR ESRTTGRNRECALPGRPENE
Sbjct: 72675 QMAQRKIRDILAQVKQHQKQSNQAQARR*PAPPCPFESRTTGRNRECALPGRPENE 72496

Query: 1448 WESGTXGPGCRSGLPT*LRKMFQ*GTLIXQPQTPTQLAQHCXPLGVSEIXAQGTFKRGLF 1627
WESGT GPGCRSGLPT*LRKMFQ*GTLI QPQTPTQLAQHC PLGVSEI AQGTFKRGLF
Sbjct: 72495 WESGTPGPGCRSGLPT*LRKMFQ*GTLISQPQTPTQLAQHCLPLGVSEILAQGTFKRGLF 72316

Query: 1628 KEALQAPPRGWITPQWEEK*NFLQVLK 1708
KEALQAPPRGWITPQWEEK*NFLQVLK
Sbjct: 72315 KEALQAPPRGWITPQWEEK*NFLQVLK 72235

Score = 303 bits (655), Expect(11) = 0.0
Identities = 130/146 (89%), Positives = 130/146 (89%)
Frame = -3 / +3

Query: 1706 LKPEGNFIFLPTEV*STLLVGPGEELL*TIHV*KCLALXFLTPRGAXSVGPIGWVFGAXRS 1527
LKPEGNFIFLPTEV*STLLVGPGEELL*TIHV*KCLAL FLTPRGA SVGPIGWVFGA RS
Sbjct: 72237 LKPEGNFIFLPTEV*STLLVGPGEELL*TIHV*KCLALEFLTPRGADSVGPIGWVFGAERS 72416

Query: 1526 GFLTGTSSFSIKWANLIYSPAXVSRIPTHSQACRGEHTLDFCPLLSWTXRDREGLVTXXXX 1347
GFLTGTSSFSIKWANLIYSPA VSRIPTHSQACRGEHTLDFCPLLSWT RDREGLVT
Sbjct: 72417 GFLTGTSSFSIKWANLIYSPAQVSRIPTHSQACRGEHTLDFCPLLSWTTRDREGLVTSSVP 72596

Query: 1346 XXXXXXSDAAA*PGPGCLGSSVEPS 1269
SDAAA*PGPGCLGSSVEPS
Sbjct: 72597 GPGYSVPSDAAA*PGPGCLGSSVEPS 72674

Score = 258 bits (557), Expect(9) = 0.0
Identities = 109/112 (97%), Positives = 109/112 (97%)
Frame = +1 / -1

Query: 1372 SLSLVQDNNNGQKSRVCSPRQA*E*VGIRDTWAGL*IRFAHLIEKDVPVRNPDLAPNTH 1551
SLSL VQDNNNGQKSRVCSPRQA*E*VGIRDTWAGL*IRFAHLIEKDVPVRNPDLAPNTH
Sbjct: 72571 SLSLRVQDNNNGQKSRVCSPRQA*E*VGIRDTWAGL*IRFAHLIEKDVPVRNPDLAPNTH 72392

Query: 1552 PIGPTLXAPRGVRNXSARHF*TWIV*RSSPGPTKRVDHTSVGRKIKFPSGFK 1707
PIGPTL APRGVRN SARHF*TWIV*RSSPGPTKRVDHTSVGRKIKFPSGFK
Sbjct: 72391 PIGPTLSAPRGVRNSSARHF*TWIV*RSSPGPTKRVDHTSVGRKIKFPSGFK 72236

Score = 232 bits (502), Expect(10) = 0.0
Identities = 95/95 (100%), Positives = 95/95 (100%)
Frame = -1 / +3

Query: 319 LGLGLFCDVADGGPLLANNNGTHILGGHQEPKGDVHLLLLGWGPRCHR*ALAGLTPrAKAP 140
LGLGLFCDVADGGPLLANNNGTHILGGHQEPKGDVHLLLLGWGPRCHR*ALAGLTPrAKAP
Sbjct: 83574 LGLGLFCDVADGGPLLANNNGTHILGGHQEPKGDVHLLLLGWGPRCHR*ALAGLTPrAKAP 83753

Query: 139 SAPILRSLCYLLIGDVGDLQGMVLQLVAIQLHDGS 35
SAPILRSLCYLLIGDVGDLQGMVLQLVAIQLHDGS
Sbjct: 83754 SAPILRSLCYLLIGDVGDLQGMVLQLVAIQLHDGS 83858

Score = 223 bits (481), Expect(10) = 0.0
Identities = 94/94 (100%), Positives = 94/94 (100%)
Frame = +2 / -3

Query: 38 AIMKLNHGHQLENHALKVSYPDEQIAQGPENGRGGFGSRGQPRQGSPPVAAGAPAKQQQV 217
AIMKLNHGHQLENHALKVSYPDEQIAQGPENGRGGFGSRGQPRQGSPPVAAGAPAKQQQV
Sbjct: 83855 AIMKLNHGHQLENHALKVSYPDEQIAQGPENGRGGFGSRGQPRQGSPPVAAGAPAKQQQV 83676

Query: 218 DIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSK 319
DIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSK
Sbjct: 83675 DIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSK 83574

Score = 177 bits (380), Expect(9) = 0.0
Identities = 68/68 (100%), Positives = 68/68 (100%)
Frame = +3 / -1

Query: 114 HRDLRMGAEGALALGVSPARHLWQRGPQPSSSKWTSPFGSWCPPSMWVPLLARRGPPSA 293
HRDLRMGAEGALALGVSPARHLWQRGPQPSSSKWTSPFGSWCPPSMWVPLLARRGPPSA
Sbjct: 83779 HRDLRMGAEGALALGVSPARHLWQRGPQPSSSKWTSPFGSWCPPSMWVPLLARRGPPSA 83600

Query: 294 TSQNRPS 317
TSQNRPS
Sbjct: 83599 TSQNRPS 83576

Score = 156 bits (336), Expect(11) = e-177
Identities = 66/82 (80%), Positives = 66/82 (80%)
Frame = -1 / +1

Query: 1513 EHLSQSSGQT*STARPCPGFPLILRPAGESTLSISARCCPGLXGTGRGWSLPPCXXXXX 1334
EHLSQSSGQT*STARPCPGFPLILRPAGESTLSISARCCPGL GTGRGWSLPPC
Sbjct: 72430 EHLSQSSGQT*STARPCPGFPLILRPAGESTLSISARCCPGLGTGRGWSLPPCLGLVT 72609

Query: 1333 XXXXXXXXXLGQDVSDLPLSHL 1268
LGQDVSDLPLSHL
Sbjct: 72610 LSLMLLLNLGQDVSDLPLSHL 72675

Score = 133 bits (286), Expect(12) = 0.0
Identities = 50/51 (98%), Positives = 50/51 (98%)
Frame = +1 / -2

Query: 31 PGSHHEAEWPPVGEPCEGGLLHPR*ADSTGT*EWAPRGLWLSGSAPPGLTC 183
P SHHEAEWPPVGEPCEGGLLHPR*ADSTGT*EWAPRGLWLSGSAPPGLTC
Sbjct: 83862 PQSHHEAEWPPVGEPCEGGLLHPR*ADSTGT*EWAPRGLWLSGSAPPGLTC 83710

Score = 128 bits (274), Expect(10) = 0.0
Identities = 46/46 (100%), Positives = 46/46 (100%)
Frame = +1 / -1

Query: 1024 GSGKNLWQTQGGELLWSQGGSEAGDPHTCASISSWPGHWQRWKNGE 1161
GSGKNLWQTQGGELLWSQGGSEAGDPHTCASISSWPGHWQRWKNGE
Sbjct: 76135 GSGKNLWQTQGGELLWSQGGSEAGDPHTCASISSWPGHWQRWKNGE 75998

Score = 124 bits (266), Expect(11) = 0.0
Identities = 48/48 (100%), Positives = 48/48 (100%)
Frame = -2 / +1

Query: 318 LDWVCFVMLRMVAPSLPIMAPTYWVGTRSRGMSTCCCLAGAPAAATGE 175
LDWVCFVMLRMVAPSLPIMAPTYWVGTRSRGMSTCCCLAGAPAAATGE
Sbjct: 83575 LDWVCFVMLRMVAPSLPIMAPTYWVGTRSRGMSTCCCLAGAPAAATGE 83718

Score = 122 bits (260), Expect(10) = 0.0
Identities = 46/46 (100%), Positives = 46/46 (100%)
Frame = -3 / +3

Query: 1160 SPFFHLCQ*PGQLMLAHVCGSPASLPPWDQRSSPP*VCHRFFPEP 1023
SPFFHLCQ*PGQLMLAHVCGSPASLPPWDQRSSPP*VCHRFFPEP
Sbjct: 75999 SPFFHLCQ*PGQLMLAHVCGSPASLPPWDQRSSPP*VCHRFFPEP 76136

Score = 116 bits (249), Expect(10) = 0.0
Identities = 46/47 (97%), Positives = 46/47 (97%)
Frame = -1 / +2

Query: 454 RFGVLSLFMHNLDHLTSGGAALRGGVHTDGFFSCTCVLLPMHVYLG 314
RFGVLSLFMHNLDHLTSGGAALRGGVHTDGFFSCTCVLLPMHVY G
Sbjct: 81932 RFGVLSLFMHNLDHLTSGGAALRGGVHTDGFFSCTCVLLPMHVYPG 82072

Score = 115 bits (246), Expect(11) = 0.0
Identities = 47/49 (95%), Positives = 47/49 (95%)
Frame = -1 / +1

Query: 1159 HRFSTFANDPASC*CWHTYVGLQLHFLLGTKEVLLLEFAIDSSLSLELG 1013
HRFSTFANDPASC*CWHTYVGLQLHFLLGTKEVLLLEFAIDSSLSL G
Sbjct: 76000 HRFSTFANDPASC*CWHTYVGLQLHFLLGTKEVLLLEFAIDSSLSLRRG 76146

Score = 115 bits (245), Expect(11) = e-177
Identities = 46/48 (95%), Positives = 46/48 (95%)
Frame = -1 / +1

Query: 1708 F*NLKEILFFFPLRCDPPSWWGLESFFKQSTFKSALRXNF*HPEGXTV 1565
F*NLKEILFFFPLRCDPPSWWGLESFFKQSTFKSALR NF*HPEG TV
Sbjct: 72235 F*NLKEILFFFPLRCDPPSWWGLESFFKQSTFKSALR*NF*HPEGQTV 72378

Score = 113 bits (242), Expect(10) = 0.0
Identities = 46/47 (97%), Positives = 46/47 (97%)
Frame = -1 / +3

Query: 712 AHGSHIILIGLPNFLHYFLLGPATILDGPLHSDGPLRVVKGKVLQRG 572
AHGSHIILIGLPNFLHYFLLGPATILDGPLHSDGPLRVVKGKVLQ G
Sbjct: 79647 AHGSHIILIGLPNFLHYFLLGPATILDGPLHSDGPLRVVKGKVLQPG 79787

Score = 110 bits (234), Expect(10) = 0.0
Identities = 45/46 (97%), Positives = 46/46 (100%)
Frame = +2 / -1

Query: 317 KIDVHRKENAGAAEKAISVHSTPEGCSSACKMILEIMHKEAKDTKT 454
+IDVHRKENAGAAEKAISVHSTPEGCSSACKMILEIMHKEAKDTKT
Sbjct: 82069 RIDVHRKENAGAAEKAISVHSTPEGCSSACKMILEIMHKEAKDTKT 81932

Score = 109 bits (232), Expect(12) = 0.0
Identities = 45/47 (95%), Positives = 47/47 (100%)
Frame = +2 / -2

Query: 1022 KAQGRIYGKLKEENFFGPKEEVKLETHIRVPASAAGRVIKGGKTVN 1162
+AQGRIYGKLKEENFFGPKEEVKLETHIRVPASAAGRVIKGGKTV+
Sbjct: 76137 QAQGRIYGKLKEENFFGPKEEVKLETHIRVPASAAGRVIKGGKTVS 75997

Score = 108 bits (230), Expect(9) = 0.0
Identities = 47/49 (95%), Positives = 47/49 (95%)
Frame = +3 / -3

Query: 1014 PNSRLREESMANSRRRTSLVPRRK*SWRPTYVCQHQQLAGSLAKVEKR* 1160
P RLREESMANSRRRTSLVPRRK*SWRPTYVCQHQQLAGSLAKVEKR*
Sbjct: 76145 PLLRLREESMANSRRRTSLVPRRK*SWRPTYVCQHQQLAGSLAKVEKR* 75999

Score = 108 bits (230), Expect(10) = 0.0
Identities = 45/45 (100%), Positives = 45/45 (100%)
Frame = +2 / -3

Query: 578 LQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS 712
LQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS
Sbjct: 79781 LQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS 79647

Score = 107 bits (228), Expect(10) = 0.0
Identities = 40/43 (93%), Positives = 42/43 (97%)
Frame = -2 / +2

Query: 948 LMEALANRESCLMCCPFLPMMAPTAWAGINTCTISCSGACIKE 820
LMEALANRESCLMCCPFLPMMAPTAWAGINTCTISCSGAC ++
Sbjct: 77939 LMEALANRESCLMCCPFLPMMAPTAWAGINTCTISCSGACCQD 78067

Score = 106 bits (227), Expect(10) = 0.0
Identities = 42/42 (100%), Positives = 42/42 (100%)
Frame = +1 / -2

Query: 454 G*RGSPEDPGP**LCRASHWQGRTEPEEGRARYRDKNHLLV 579
G*RGSPEDPGP**LCRASHWQGRTEPEEGRARYRDKNHLLV
Sbjct: 80646 G*RGSPEDPGP**LCRASHWQGRTEPEEGRARYRDKNHLLV 80521

Score = 106 bits (227), Expect(12) = 0.0
Identities = 45/46 (97%), Positives = 45/46 (97%)
Frame = +3 / -1

Query: 573 PRCKTLPFTTLRGPSL*RGPSRIVAGPSRK**RKFGPRMMWLP* 710
P CKTLPFTTLRGPSL*RGPSRIVAGPSRK**RKFGPRMMWLP*
Sbjct: 79786 PGCKTLPFTTLRGPSL*RGPSRIVAGPSRK**RKFGPRMMWLP* 79649

Score = 105 bits (224), Expect(10) = 0.0
Identities = 41/43 (95%), Positives = 42/43 (97%)
Frame = +1 / -1

Query: 820 LLYAGSRAGDGAGVYPRPGSGRHHRQEGAAHQ TALPVCQRLHQ 948
+L AGSRAGDGAGVYPRPGSGRHHRQEGAAHQ TALPVCQRLHQ
Sbjct: 78067 ILAAGSRAGDGAGVYPRPGSGRHHRQEGAAHQ TALPVCQRLHQ 77939

Score = 103 bits (219), Expect(10) = 0.0
Identities = 42/42 (100%), Positives = 42/42 (100%)
Frame = -3 / +2

Query: 578 TRRW*FLSRYLALPSSGSLVPCQ*DALQSYYPGSSGEPRQP 453
TRRW*FLSRYLALPSSGSLVPCQ*DALQSYYPGSSGEPRQP
Sbjct: 80522 TRRW*FLSRYLALPSSGSLVPCQ*DALQSYYPGSSGEPRQP 80647

Score = 103 bits (219), Expect(10) = 0.0
Identities = 38/38 (100%), Positives = 38/38 (100%)
Frame = +1 / -2

Query: 715 SPDPWPEPGCCRSFPSFIQRSPAASQORYWGCSL*LLY 828
SPDPWPEPGCCRSFPSFIQRSPAASQORYWGCSL*LLY
Sbjct: 78588 SPDPWPEPGCCRSFPSFIQRSPAASQORYWGCSL*LLY 78475

Score = 100 bits (213), Expect(11) = 0.0
Identities = 41/41 (100%), Positives = 41/41 (100%)
Frame = -1 / +3

Query: 577 RGDGDFCLGILLYLLQVPSFLANETPYKVIMQDLQGNLVS 455
RGDGDFCLGILLYLLQVPSFLANETPYKVIMQDLQGNLVS
Sbjct: 80523 RGDGDFCLGILLYLLQVPSFLANETPYKVIMQDLQGNLVS 80645

Score = 100 bits (212), Expect(11) = 0.0
Identities = 45/45 (100%), Positives = 45/45 (100%)
Frame = -2 / +1

Query: 711 LMAATSFS*ASRTFFIISCSALQQFSMAPFTVMVLSGL*RVRSCN 577
LMAATSFS*ASRTFFIISCSALQQFSMAPFTVMVLSGL*RVRSCN
Sbjct: 79648 LMAATSFS*ASRTFFIISCSALQQFSMAPFTVMVLSGL*RVRSCN 79782

Score = 96.8 bits (205), Expect(10) = 0.0
Identities = 38/39 (97%), Positives = 39/39 (100%)
Frame = -1 / +3

Query: 1273 HLTGIEMSDDFHDDLVLIRGLVSWYYHLSCRQILQLVH 1157
+LTGIEMSDDFHDDLVLIRGLVSWYYHLSCRQILQLVH
Sbjct: 75648 YLTGIEMSDDFHDDLVLIRGLVSWYYHLSCRQILQLVH 75764

Score = 96.4 bits (204), Expect(12) = 0.0
Identities = 41/41 (100%), Positives = 41/41 (100%)
Frame = +2 / -3

Query: 455 ADEVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITISS 577
ADEVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITISS
Sbjct: 80645 ADEVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITISS 80523

Score = 95.5 bits (202), Expect(12) = 0.0
Identities = 41/44 (93%), Positives = 43/44 (97%)
Frame = +2 / -2

Query: 821 SFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKI 952
S+ QAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASASIK+
Sbjct: 78066 SWQQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKV 77935

Score = 95.0 bits (201), Expect = 7e-17
Identities = 40/49 (81%), Positives = 41/49 (83%)
Frame = -3 / +2

Query: 1301 PGCLGSSVEPSDWHNRNVR*FSR*PGRSHQSGLLVLPPQLPSNSATRSP 1155
P G + DWHNRNVR*FSR*PGRSHQSGLLVLPPQLPSNSATRSP
Sbjct: 75620 PSLNGGAPYPVDWHNRNVR*FSR*PGRSHQSGLLVLPPQLPSNSATRSP 75766

Score = 94.1 bits (199), Expect(11) = e-177
Identities = 38/38 (100%), Positives = 38/38 (100%)
Frame = -2 / +1

Query: 576 EEMVIFVSVSCSTFFRFRPSLPMRRPTKLLWARIFRGT 463
EEMVIFVSVSCSTFFRFRPSLPMRRPTKLLWARIFRGT
Sbjct: 80524 EEMVIFVSVSCSTFFRFRPSLPMRRPTKLLWARIFRGT 80637

Score = 93.6 bits (198), Expect(10) = 0.0
Identities = 38/38 (100%), Positives = 38/38 (100%)
Frame = +1 / -2

Query: 1156 GERVAEFDGS*GGSTKRPDP**ERPGHRENHRTFLCQS 1269
GERVAEFDGS*GGSTKRPDP**ERPGHRENHRTFLCQS
Sbjct: 75765 GERVAEFDGS*GGSTKRPDP**ERPGHRENHRTFLCQS 75652

Score = 93.2 bits (197), Expect(11) = 0.0
Identities = 38/38 (100%), Positives = 38/38 (100%)
Frame = -2 / +1

Query: 1269 *LA*KCPMIFTMTWSFSSGVWSLGTSTSAVKFCNSFT 1156
*LA*KCPMIFTMTWSFSSGVWSLGTSTSAVKFCNSFT
Sbjct: 75652 *LA*KCPMIFTMTWSFSSGVWSLGTSTSAVKFCNSFT 75765

Score = 92.7 bits (196), Expect(9) = 0.0
Identities = 41/41 (100%), Positives = 41/41 (100%)
Frame = +3 / -1

Query: 456 LTRFP*RSWPIITL*GVSLARKDGT*RR*SKIPRQKSPSPR 578
LTRFP*RSWPIITL*GVSLARKDGT*RR*SKIPRQKSPSPR
Sbjct: 80644 LTRFP*RSWPIITL*GVSLARKDGT*RR*SKIPRQKSPSPR 80522

Score = 92.2 bits (195), Expect(12) = 0.0
Identities = 39/43 (90%), Positives = 40/43 (93%)
Frame = +2 / -3

Query: 1145 GGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQM 1273
G VNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQ+
Sbjct: 75776 GHPQVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQV 75648

Score = 90.0 bits (190), Expect(11) = 0.0
Identities = 38/38 (100%), Positives = 38/38 (100%)
Frame = -2 / +3

Query: 429 CIISKIILQAEEQPSGVECTLMAFSAAPAFSFLCTSIL 316
CIISKIILQAEEQPSGVECTLMAFSAAPAFSFLCTSIL
Sbjct: 81957 CIISKIILQAEEQPSGVECTLMAFSAAPAFSFLCTSIL 82070

Score = 89.5 bits (189), Expect(9) = 0.0
Identities = 39/41 (95%), Positives = 41/41 (100%)
Frame = +3 / -1

Query: 1155 R*TSCRI*RQLRW*YQETRPLMRTRRSS*KSSDISMPVRWL 1277
R*TSCRI*RQLRW*YQETRPLMRTRRSS*KSSDISMPVR++
Sbjct: 75766 R*TSCRI*RQLRW*YQETRPLMRTRRSS*KSSDISMPVRYI 75644

Score = 88.1 bits (186), Expect(10) = 0.0
Identities = 38/39 (97%), Positives = 39/39 (100%)
Frame = -2 / +1

Query: 828 IKEL*GAAPVTLLGGGGTALDEAGKRPTAARFRPGIR*E 712
IKEL*GAAPVTLLGGGGTALDEAGKRPTAARFRPGIR*+
Sbjct: 78475 IKEL*GAAPVTLLGGGGTALDEAGKRPTAARFRPGIR*D 78591

Score = 86.3 bits (182), Expect(11) = 0.0
Identities = 36/36 (100%), Positives = 36/36 (100%)
Frame = -1 / +3

Query: 820 AIGSSPSNAAGRRRDCAG*SWEKTYSSQVQARDQVR 713
AIGSSPSNAAGRRRDCAG*SWEKTYSSQVQARDQVR
Sbjct: 78483 AIGSSPSNAAGRRRDCAG*SWEKTYSSQVQARDQVR 78590

Score = 85.8 bits (181), Expect(11) = e-177
Identities = 35/49 (71%), Positives = 35/49 (71%)
Frame = -3 / +1

Query: 461 RQPFWCP*PLYAXXXXXXXXXXXXXPQGWSAH*WLFQLHLRSPSYARLSW 315
R FWCP*PLYA PQGWSAH*WLFQLHLRSPSYARLSW
Sbjct: 81925 RLTFWCP*PLYA*SPRSSYKRRSSPQGWSAH*WLFQLHLRSPSYARLSW 82071

Score = 85.4 bits (180), Expect(11) = 0.0
Identities = 31/31 (100%), Positives = 31/31 (100%)
Frame = -2 / +1

Query: 129 FSGPCAICSSGM*ETFRAWFSNWWPFSFMMA 37
FSGPCAICSSGM*ETFRAWFSNWWPFSFMMA
Sbjct: 83764 FSGPCAICSSGM*ETFRAWFSNWWPFSFMMA 83856

Score = 82.2 bits (173), Expect(11) = e-177
Identities = 36/51 (70%), Positives = 36/51 (70%)
Frame = -3 / +2

Query: 182 QVSPGGADPESQSPLGAHSQVPVLSAHRGCRRXXXXXXXXXXXXX*WLP G 30
QVSPGGADPESQSPLGAHSQVPVLSAHRGCRR *W L G
Sbjct: 83711 QVSPGGADPESQSPLGAHSQVPVLSAHRGCRRPSGHGSPTGGHSAS*WLWG 83863

Score = 79.0 bits (166), Expect(11) = e-177
Identities = 33/42 (78%), Positives = 33/42 (78%)
Frame = -3 / +2

Query: 701 PHHSHRPPELSSLFPARPCNNSRXXXXXXXXXXQGCKG*GLAT 576
PHHSHRPPELSSLFPARPCNNSR QGCKG*GLAT
Sbjct: 79658 PHHSHRPPELSSLFPARPCNNSRWPPSQ*WSSQGCKG*GLAT 79783

Score = 77.6 bits (163), Expect(11) = 0.0
Identities = 30/30 (100%), Positives = 30/30 (100%)
Frame = -3 / +3

Query: 947 *WRRWQTGRAV*CAAPSCR*WRPLPGRG*T 858
*WRRWQTGRAV*CAAPSCR*WRPLPGRG*T
Sbjct: 77940 *WRRWQTGRAV*CAAPSCR*WRPLPGRG*T 78029



Your request has been successfully submitted and put into the Blast Queue.

Query = (1708 letters)

SEQ 5
translated → translation
dp
(blastx)

The request ID is

or

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ Linkout ☐ Sequence Retrieval ☒ NCBI-gi in

Number of: Descriptions Alignments

Alignment view

Limit results by or select from:

Expect value range:



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

SEQ 5
gi 4191607 (IGFII)

Sequence 1 lcl|seq_1 Length 1708 (1 .. 1708)

Sequence 2 lcl|seq_2 Length 2130 (1 .. 2130)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 3163 bits (1645), Expect = 0.0
 Identities = 1667/1678 (99%), Gaps = 6/1678 (0%)
 Strand = Plus / Plus

```

Query: 37   agccatcatgaagctgaatggccaccagttggagaaccatgccctgaaggtctcctacat 96
           |||
Sbjct: 411  agccatcatgaagctgaatggccaccagttggagaaccatgccctgaaggtctcctacat 470

Query: 97   ccccgatgagcagatagcacagggacctgagaatggcgccgagggggctttggctctcg 156
           |||
Sbjct: 471  ccccgatgagcagatagcacagggacctgagaatggcgccgagggggctttggctctcg 530

Query: 157  gggtcagccccgccagggtcacctgtggcagcgggggccccagccaagcagcagcaagt 216
           |||
Sbjct: 531  gggtcagccccgccagggtcacctgtggcagcgggggccccagccaagcagcagcaagt 590

Query: 217  ggacatcccccttcgggtcctggtgccaccagtatgtgggtgccattattggcaagga 276
           |||
Sbjct: 591  ggacatcccccttcgggtcctggtgccaccagtatgtgggtgccattattggcaagga 650

Query: 277  gggggccaccatccgcaacatcacaaaacagaccagtcgaagatagacgtgcataggaa 336
           |||
  
```

Sbjct: 651 gggggccaccatccgcaacatcacaaaacagaccaggtccaagatagacgtgcataggaa 710

Query: 337 ggagaacgcaggtgcagctgaaaaagccatcagtggtgcactccaccctgagggctgctc 396
|||||
Sbjct: 711 ggagaacgcaggtgcagctgaaaaagccatcagtggtgcactccaccctgagggctgctc 770

Query: 397 ctccgcttgtaagatgatcttgagattatgcataaagaggctaaggacacccaaaacggc 456
|||||
Sbjct: 771 ctccgcttgtaagatgatcttgagattatgcataaagaggctaaggacacccaaaacggc 830

Query: 457 tgacgaggttcccctgaagatcctggcccataataactttgtagggcgctctcattggcaa 516
|||||
Sbjct: 831 tgacgaggttcccctgaagatcctggcccataataactttgtagggcgctctcattggcaa 890

Query: 517 ggaaggacggaacctgaagaaggtagagcaagataccgagacaaaaatcaccatctcctc 576
|||||
Sbjct: 891 ggaaggacggaacctgaagaaggtagagcaagataccgagacaaaaatcaccatctcctc 950

Query: 577 gttgcaagaccttaccctttacaaccctgagaggaccatcactgtgaagggggccatcga 636
|||||
Sbjct: 951 gttgcaagaccttaccctttacaaccctgagaggaccatcactgtgaagggggccatcga 1010

Query: 637 gaattgttgaggccgagcaggaaataatgaagaaagttcgggaggcctatgagaatga 696
|||||
Sbjct: 1011 gaattgttgaggccgagcaggaaataatgaagaaagttcgggaggcctatgagaatga 1070

Query: 697 tgtggctgcatgagc-----tctcacctgatccctggcctgaacctggctgctgtagg 750
|||||
Sbjct: 1071 tgtggctgcatgagcctgcagctctcacctgatccctggcctgaacctggctgctgtagg 1130

Query: 751 tcttttcccagcttcatccagcgcagtcgccgcctcccagcagcggttactggggctgc 810
|||||
Sbjct: 1131 tcttttcccagcttcatccagcgcagtcgccgcctcccagcagcggttactggggctgc 1190

Query: 811 tccctatagctcctttatgcaggctcccgagcaggagatggtgcaggtgtttatccccgc 870
|||||
Sbjct: 1191 tccctatagctcctttatgcaggctcccgagcaggagatggtgcaggtgtttatccccgc 1250

Query: 871 ccaggcagtgggcgccatcatcggaagaaggggcagcacatcaaacagctctcccgggt 930
|||||
Sbjct: 1251 ccaggcagtgggcgccatcatcggaagaaggggcagcacatcaaacagctctcccgggt 1310

Query: 931 tgccagcgctccatcaagattgcaccaccgaaacacctgactccaaagttcgtatggt 990
|||||
Sbjct: 1311 tgccagcgctccatcaagattgcaccaccgaaacacctgactccaaagttcgtatggt 1370

Query: 991 tatcatcactggaccgccagaggcccaattcaaggctcaggaagaatctatggcaaact 1050
|||||
Sbjct: 1371 tatcatcactggaccgccagaggcccaattcaaggctcaggaagaatctatggcaaact 1430

Query: 1051 caaggaggagaacttctttgggcccaaggaggaagtgaagctggagaccacatacgtgt 1110
|||||

Sbjct: 1431 caaggaggagaacttctttggtcccaaggaggaagtgaagctggagacccacatacgtgt 1490

Query: 1111 gccagcatcagcagctggccgggtcattggcaaaggtggaaaaacggtgaacgagttgca 1170
|||||
Sbjct: 1491 gccagcatcagcagctggccgggtcattggcaaaggtggaaaaacggtgaacgagttgca 1550

Query: 1171 gaatttgacggcagctgaggtggttagtaccaagagaccagaccctgatgagaacgacca 1230
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Sbjct: 1551 gaatttgacggcagctgaggtggttagtaccaagagaccagaccctgatgagaacgacca 1610

Query: 1231 ggtcatcgtgaaaatcatcggacatttctatgccagtcagatggctcaacggaagatccg 1290
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Sbjct: 1611 ggtcatcgtgaaaatcatcggacatttctatgccagtcagatggctcaacggaagatccg 1670

Query: 1291 agacatcctggcccaggttaagcagcagcatcagaaggacagagtaaccaggcccaggc 1350
|||||
Sbjct: 1671 agacatcctggcccaggttaagcagcagcatcagaaggacagagtaaccaggcccaggc 1730

Query: 1351 acggaggaagtgaccagcccctcctgtcccttgcagtcaggacaacaacgggcagaaa 1410
|||||
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Query: 1411 tcgagagtgtgctctccccggcaggcctgagaatgagtgggaatccgggacacctggggcc 1470
|||||
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Query: 1471 gggctgtagatcaggtttgccacttgattgagaaagatgttcagtgaggaaccctgat 1530
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Query: 1531 ctctcagccccaaacacccacccaattggcccaacactgtctgccctcgggggtgtcaga 1590
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Sbjct: 1911 ctctcagccccaaacacccacccaattggcccaacactgtctgccctcgggggtgtcaga 1970

Query: 1591 aattttagcgcaaggcacttttaaacgtggattgtttaagaagctctccaggccccacc 1650
|||||
Sbjct: 1971 aattttagcgcaaggcacttttaaacgtggattgtttaagaagctctccaggccccacc 2030

Query: 1651 aagaggggtggatcacacctcagtgggaagaaaaataaaatttccttcagggttttaaaa 1708
|||||
Sbjct: 2031 aagaggggtggatcacacctcagtgggaagaaaaataaaatttccttcagggttttaaaa 2088

CPU time: 0.01 user secs. 0.02 sys. secs 0.03 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 12

Number of Sequences: 0
Number of extensions: 12
Number of successful extensions: 2
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 1708
length of database: 8,918,056,233
effective HSP length: 25
effective length of query: 1683
effective length of database: 8,918,056,208
effective search space: 15009088598064
effective search space used: 15009088598064
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)



results of BLAST

BLASTN 2.2.6 [Apr-09-2003]

RID: 1061911853-27554-2290282.BLASTQ3

Database: All GenBank+EMBL+DBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)
1,886,208 sequences; 8,918,056,233 total letters

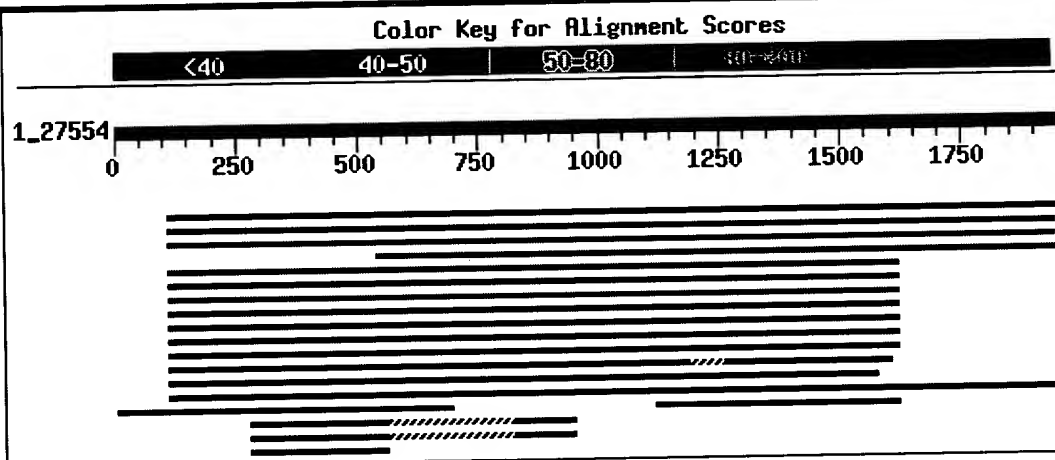
seq 7

Taxonomy reports

Query=
(1946 letters)

Distribution of 39 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score E
(bits) Value

gi 4191607 gb AF117106.1 AF117106	Homo sapiens IGF-II mRNA-...	3488	0.0
gi 21361351 ref NM_006546.2	Homo sapiens IGF-II mRNA-bind...	3451	0.0
gi 7141071 gb AF198254.1 AF198254	Homo sapiens mRNA-binding...	3451	0.0
gi 22760672 dbj AK074915.1	Homo sapiens cDNA FLJ90434 fis...	2663	0.0
gi 31342209 ref NM_175594.2	Rattus norvegicus IGF-II mRNA-...	1950	0.0
gi 27464837 gb AF541940.1	Rattus norvegicus b-actin zipcod...	1950	0.0
gi 3273748 gb AF061569.1 AF061569	Mus musculus coding regio...	1892	0.0
gi 31560605 ref NM_009951.2	Mus musculus insulin-like grow...	1886	0.0
gi 12851513 dbj AK013940.1	Mus musculus 13 days embryo hea...	1886	0.0
gi 26336870 dbj AK044850.1	Mus musculus 9.5 days embryo pa...	1886	0.0
gi 30354043 gb BC051679.1	Mus musculus insulin-like growth...	1886	0.0
gi 27689046 ref XM_220886.1	Rattus norvegicus similar to I...	1367	0.0
gi 2570920 gb AF026527.1 AF026527	Gallus gallus zipcode-bin...	1327	0.0
gi 24580458 gb AC105030.11	Homo sapiens chromosome 17, clo...	829	0.0
gi 21637524 gb AC091133.11	Homo sapiens chromosome 17, clo...	544	e-151
gi 30581644 gb AC094527.7	Rattus norvegicus 5 BAC CH230-4L...	477	e-131
gi 21954991 gb AC098642.5	Genomic sequence for Mus musculu...	342	1e-90

gi 14475918 gb AC084407.10	Mus Musculus Strain C57BL6/J Ch...	342	1e-90
gi 22204252 emb AL606704.20	Mouse DNA sequence from clone ...	342	1e-90

Alignments

>gi|4191607|gb|AF117106.1|AF117106 Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1)
Length = 2130

Score = 3488 bits (1814), Expect = 0.0
Identities = 1834/1845 (99%), Gaps = 6/1845 (0%)
Strand = Plus / Plus

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Sbjct: 244  aggagccggaattcaaatccgaaatattccacccagctccgatgggaagtactggac 303

Query: 168  agcctgctggctcagtatggtacagtagagaactgtgagcaagtgaacaccgagagtgag 227
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Sbjct: 304  agcctgctggctcagtatggtacagtagagaactgtgagcaagtgaacaccgagagtgag 363

Query: 228  acggcagtggtgaatgtcacctattccaaccgggagcagaccaggcaagccatcatgaag 287
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Sbjct: 364  acggcagtggtgaatgtcacctattccaaccgggagcagaccaggcaagccatcatgaag 423

Query: 288  ctgaatggccaccagttggagaacctatgcctgaaggtctcctacatccccgatgagcag 347
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Sbjct: 424  ctgaatggccaccagttggagaacctatgcctgaaggtctcctacatccccgatgagcag 483

Query: 348  atagcacagggacctgagaatgggcgccgagggggctttggctctcggggtcagccccgc 407
          |||
Sbjct: 484  atagcacagggacctgagaatgggcgccgagggggctttggctctcggggtcagccccgc 543

Query: 408  cagggctcacctgtggcagcgggggccccagccaagcagcagcaagtggacatccccctt 467
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Sbjct: 544  cagggctcacctgtggcagcgggggccccagccaagcagcagcaagtggacatccccctt 603

Query: 468  cggctcctggtgcccaccagtatgtgggtgccattattggcaaggagggggccaccatc 527
          |||
Sbjct: 604  cggctcctggtgcccaccagtatgtgggtgccattattggcaaggagggggccaccatc 663

Query: 528  cgcaacatcacaaaacagacccagtcgaagatagacgtgcataggaaggagaacgcaggt 587
          |||
Sbjct: 664  cgcaacatcacaaaacagacccagtcgaagatagacgtgcataggaaggagaacgcaggt 723

Query: 588  gcagctgaaaaagccatcagtgtgcactccaccctgagggctgctcctccgcttgaag 647
          |||
Sbjct: 724  gcagctgaaaaagccatcagtgtgcactccaccctgagggctgctcctccgcttgaag 783

Query: 648  atgatcttgagattatgcataaagaggctaaggacacccaaaacggctgacgaggttccc 707
          |||
Sbjct: 784  atgatcttgagattatgcataaagaggctaaggacacccaaaacggctgacgaggttccc 843

Query: 708  ctgaagatcctggccataataactttgtagggcggtctcattggcaaggaaggacggaac 767
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Sbjct: 844 ctgaagatcctggcccataataactttgtagggcgtctcattggcaaggaaggacggaac 903

Query: 768 ctgaagaaggtagagcaagataccgagacaaaaatcaccatctcctcggtgcaagacctt 827
|||||

Sbjct: 904 ctgaagaaggtagagcaagataccgagacaaaaatcaccatctcctcggtgcaagacctt 963

Query: 828 accctttacaaccctgagaggaccatcactgtgaagggggccatcgagaattggtgcagg 887
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Sbjct: 964 accctttacaaccctgagaggaccatcactgtgaagggggccatcgagaattggtgcagg 1023

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|||||

Sbjct: 1024 gccgagcaggaaataatgaagaaagttcgggaggcctatgagaatgatgtggctgccatg 1083

Query: 948 a^f--gc--tctcacctgatccctggcctgaacctggctgctgtaggtcttttcccagct 1001
| |||

Sbjct: 1084 agcctgcagtctcacctgatccctggcctgaacctggctgctgtaggtcttttcccagct 1143

Query: 1002 tcatccagcgcagtcctcgccgctcccagcagcgttactggggctgctccctatagctcc 1061
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Sbjct: 1144 tcatccagcgcagtcctcgccgctcccagcagcgttactggggctgctccctatagctcc 1203

Query: 1062 tttatgcaggctcccagcaggagatggtgcagggtgttatccccgcccaggcagtgggc 1121
|||||

Sbjct: 1204 tttatgcaggctcccagcaggagatggtgcagggtgttatccccgcccaggcagtgggc 1263

Query: 1122 gccatcatcggcaagaaggggcagcacatcaaacagctctcccggtttgccagcgcctcc 1181
|||||

Sbjct: 1264 gccatcatcggcaagaaggggcagcacatcaaacagctctcccggtttgccagcgcctcc 1323

Query: 1182 atcaagattgcaccacccgaaacacctgactccaaagttcgtatgggttatcatcactgga 1241
|||||

Sbjct: 1324 atcaagattgcaccacccgaaacacctgactccaaagttcgtatgggttatcatcactgga 1383

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Query: 1302 ttctttggtcccaaggaggaagtgaagctggagacccacatacgtgtgccagcatcagca 1361
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Sbjct: 1444 ttctttggtcccaaggaggaagtgaagctggagacccacatacgtgtgccagcatcagca 1503

Query: 1362 gctggccgggtcatttgcaaaaggtggaaaaacggtgaacgagttgcagaatttgacggca 1421
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Sbjct: 1684 caggttaagcagcagcatcagaagggacagagtaaccaggcccaggcacggaggaagtga 1743

Query: 1602 ccagccccctccctgtcccttngagtccaggacaacaacgggcagaaatcgagagtgtgct 1661
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Sbjct: 1744 ccagccccctccctgtcccttcgagtccaggacaacaacgggcagaaatcgagagtgtgct 1803

Query: 1662 ctccccggcaggcctgagaatgagtgggaatccgggacacntgggccgggctgtagatca 1721
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Sbjct: 1984 ggcacttttaaacgtggattgtttaagaagctctccaggccccaccaagagggtggatc 2043

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Identities = 1826/1842 (99%), Gaps = 7/1842 (0%)
Strand = Plus / Plus

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Query: 168 agcctgctggctcagtatggtacagtagagaactgtgagcaagtgaacaccgagagtgag 227
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Sbjct: 600 agcctgctggctcagtatggtacagtagagaactgtgagcaagtgaacaccgagagtgag 659

Query: 228 acggcagtggtgaatgtcacctattccaacggggagcagaccaggcaagccatcatgaag 287
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Sbjct: 660 acggcagtggtgaatgtcacctattccaacggggagcagaccaggcaagccatcatgaag 719

Query: 288 ctgaatggccaccagttggagaacctatgccctgaagggtctcctacatccccgatgagcag 347
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Sbjct: 720 ctgaatggccaccagttggagaacctatgccctgaagggtctcctacatccccgatgagcag 779

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Sbjct: 780 atagcacaggacctgagaatggcgccgagggggctttggctctcggggtcagccccgc 839

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Sbjct: 840 cagggtcacctgtggcagcggggggccccagccaagcagcagcaagtggacatccccctt 899

Query: 468 cggtcctggtgcccacccagtatgtgggtgccattattggcaaggagggggccaccatc 527
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Sbjct: 900 cggtcctggtgcccacccagtatgtgggtgccattattggcaaggagggggccaccatc 959

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Sbjct: 960 cgcaacatcacaaaacagaccagtcgaagatagacgtgcataggaaggagaacgcaggt 1019

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>gi|7141071|gb|AF198254.1|AF198254 Homo sapiens mRNA-binding protein CRDBP mRNA, com
Length = 2381

Score = 3451 bits (1795), Expect = 0.0
Identities = 1826/1842 (99%), Gaps = 7/1842 (0%)
Strand = Plus / Plus

Query: 108 aggagccggaaaattcaaattccgaaatattccacccagctccgatgggaagtactggac 167
|||||
Sbjct: 540 aggagccggaaaattcaaattccgaaatattccacccagctccgatgggaagtactggac 599

Query: 168 agcctgctggctcagtattggtacagtagagaactgtgagcaagtgaacaccgagagtggag 227
|||||
Sbjct: 600 agcctgctggctcagtattggtacagtagagaactgtgagcaagtgaacaccgagagtggag 659

Query: 228 acggcagtggtgaatgtcacctattccaacgggagcagaccaggcaagccatcatgaag 287
|||||
Sbjct: 660 acggcagtggtgaatgtcacctattccaacgggagcagaccaggcaagccatcatgaag 719

Query: 288 ctgaatggccaccagttggagaacctatgcctgaaggtctcctacatccccgatgagcag 347
|||||
Sbjct: 720 ctgaatggccaccagttggagaacctatgcctgaaggtctcctacatccccgatgagcag 779

Query: 348 atagcacagggacctgagaatgggcgcccagggggccttggctctcggggtcagccccgc 407
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Sbjct: 780 atagcacagggacctgagaatgggcgcccagggggccttggctctcggggtcagccccgc 839

Query: 408 cagggctcacctgtggcagcgggggccccagccaagcagcagcaagtggacatccccctt 467
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Sbjct: 840 cagggctcacctgtggcagcgggggccccagccaagcagcagcaagtggacatccccctt 899

Query: 468 cggctcctggtgcccacccagttatgtgggtgccattattggcaaggagggggccaccatc 527
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Sbjct: 900 cggctcctggtgcccacccagttatgtgggtgccattattggcaaggagggggccaccatc 959

Query: 528 cgcaacatcacaaaacagaccagtcgaagatagacgtgcataggaaggagaacgcaggt 587
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>gi|22760672|dbj|AK074915.1| Homo sapiens cDNA FLJ90434 fis, clone NT2RP3000789, hig
Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1) mRNA
Length = 2780

Score = 2663 bits (1385), Expect = 0.0
Identities = 1405/1416 (99%), Gaps = 6/1416 (0%)
Strand = Plus / Plus

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|||||
Sbjct: 1 acaaaacagaccagtcgaagatagacgtgcataggaaggagaacgcaggtgcagctgaa 60

Query: 597 aaagccatcagtgtgcactccaccctgagggtgctcctccgcttgtaagatgatcttg 656
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Sbjct: 121 gagattatgcataaagaggctaaggacaccaaacggctgacgaggttcccctgaagatc 180

Query: 717 ctggcccataataactttgtagggcgtctcattggcaaggaaggacggaacctgaagaag 776
|||||
Sbjct: 181 ctggcccataataactttgtagggcgtctcattggcaaggaaggacggaacctgaagaag 240

Query: 777 gtagagcaagataccgagacaaaaatcaccatctcctcggttgcaagaccttaccctttac 836
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Query: 837 aaccctgagaggaccatcactgtgaagggggccatcgagaattggtgcagggccgagcag 896
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Sbjct: 361 gaaataatgaagaaagttcgggaggcctatgagaatgatgtggctgccatgagcctgcag 420

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Query: 1671 aggcctgagaatgagtgggaatccgggacacntgggcccgggctgtagatcaggtttgccc 1730
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Query: 1791 caattggcccaacactgtntgccctcgggggtgtcagaaattntagcgcaaggcactttt 1850
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Sbjct: 1321 aaacgtggattgtttaaagaagctctccaggccccaccaagagggtggatcacacctcag 1380

Query: 1911 tgggaagaaaaataaaatttccttcaggttttaaaa 1946
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Sbjct: 1381 tgggaagaaaaataaaatttccttcaggttttaaaa 1416

>gi|31342209|ref|NM_175594.2| Rattus norvegicus IGF-II mRNA-binding protein 1 (Imp-1)
Length = 2105

Score = 1950 bits (1014), Expect = 0.0
Identities = 1352/1519 (89%), Gaps = 7/1519 (0%)
Strand = Plus / Plus

Query: 108 aggagccggaaaaattcaaatccgaaatattccaccccagctccgatgggaagtactggac 167
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Sbjct: 457 aggagtcggaataacagatccggaatattccacctcagctccgatgggaagtgtggtat 516

Query: 168 agcctgctggctcagtatggtacagtagagaactgtgagcaagtgaacaccgagagttag 227
|||||
Sbjct: 517 agccttctggcccagtagcggcacagtgggagaactgtgagcaagtgaacaccgagagttag 576

Query: 228 acggcagtggtgaatgtcacctattccaacggggagcagaccaggcaagccatcatgaag 287
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Sbjct: 577 acggcgggtggtcaacgtcacctactctaaccggggagcagaccaggcaagccatcatgaag 636

Query: 288 ctgaatggccaccagttggagaaccatgccctgaagggtctcctacatccccgatgagcag 347
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Sbjct: 637 ctaaatggccatcaactggagaaccatgccctgaagggtttcctacatacctgatgagcag 696

Query: 348 atagcacagggacctgagaatgggcgcccagggggctttgggtctcgggggtcagccccgc 407
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Query: 408 cagggctcacctgtggcagcggggccccagccaagcagcagcaagtggacatccccctt 467
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Sbjct: 817 cggtccttggtgcccacgcagtatgtaggcgccatcattggcaaggaggggtgccaccatc 876

Query: 528 cgcaacatcacaaaacagacctcgaagatagacgtgcataggaaggagaacgcaggt 587
Sbjct: 877 cgaaacatcacaaaacagactcagtcgaagatagacgtgcacaggaaggagaacgcgggg 936

Query: 588 gcagctgaaaaagccatcagtgctgactccaccctgagggctgctcctcgcttctaag 647
Sbjct: 937 gctgcggagaaggccatcagtgctgactcgaccctgaaggctgctcctcggcctctaag 996

Query: 648 atgatcttgagattatgcataaagaggctaaggacaccaaagcggtgacgaggttccc 707
Sbjct: 997 atgatcttgagattatgcacaaggaggcaaaggacaccaagacggcagacgaagttccc 1056

Query: 708 ctgaagatcctggcccataataactttgtagggcgctctcattggcaaggaaggacggaac 767
Sbjct: 1057 ctgaagatcctgggtcataataacttcgtggggcgactcattggaaaggaagggcggaac 1116

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Query: 828 accctttaacaacctgagaggaccatcactgtgaagggggccatcgagaattgttgacagg 887
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Query: 1122 gccatcatcggcaagaaggggcagcacatcaaacagctctcccgtttgccagcgcctcc 1181
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Sbjct: 1537 atcaagattgctccaccagaaacacctgactccaaagttcgaatggtgtcatcactgga 1596

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Sbjct: 1777 gccgaggtggtcgtgccgagagaccagacccagacgagaacgaccaagtcattgttaag 1836

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Sbjct: 1837 atcatcggacatttctatgccagtcagatggcccagcggaagatccgagacatcctggct 1896

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Sbjct: 1897 caaggttaagcagcagcaccagaagggacagagcaaccaggcccaggcacgaaggaagtga 1956

Query: 1602 cca-gcccctccctgtccc 1619
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>gi|27464837|gb|AF541940.1| Rattus norvegicus b-actin zipcode binding protein 1 mRNA
cds
Length = 2105

Score = 1950 bits (1014), Expect = 0.0
Identities = 1352/1519 (89%), Gaps = 7/1519 (0%)
Strand = Plus / Plus

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Query: 168 agcctgctgggtcagtatggtacagtagagaactgtgagcaagtgaacaccgagagtgag 227
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Sbjct: 517 agccttctggcccagtagggcacagtggagaactgtgagcaagtgaacaccgagagtgag 576

Query: 228 acggcagtggtgaatgtcacctattccaaccgggagcagaccaggcaagccatcatgaag 287
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Sbjct: 577 acggcgggtggtcaacgtcacctactctaaccgggagcagaccaggcaagccatcatgaag 636

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Query: 348 atagcacagggacctgagaatggcgccgagggggctttggctctcggggtcagccccgc 407
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Query: 408 cagggtcacctgtggcagcgggggccccagccaagcagcagcaagtggacatccccctt 467
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Sbjct: 1897 caagttaagcagcagcaccagaaggacagagcaaccaggcccaggcacgaaggaagtga 1956

Query: 1602 cca-gccccctccctgtccc 1619
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>gi|3273748|gb|AF061569.1|AF061569 Mus musculus coding region determinant binding pr
cds
Length = 2223

Score = 1892 bits (984), Expect = 0.0
Identities = 1345/1522 (88%), Gaps = 13/1522 (0%)
Strand = Plus / Plus

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|| |||||
Sbjct: 365 aggagtcggaaaatacagatccgcaatattccacctcagctccgatgggaagtgttagat 424

Query: 168 agcctgctggctcagtatggtacagtagagaactgtgagcaagtgaacaccgagagtgag 227
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|||

Sbjct: 1324 cttcatgcaggctccggagcaggagatgggtacaagtgttcatccccgcccaggctgtggg 1383

Query: 1121 cgccatcatcggcaagaaggggcagcacatcaaacagctctcccggtt-gccagcgcct 1179
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Sbjct: 1384 cgccatcattggcaagaagggccagcacatcaaacaactctcccg-tttcgccagcgcct 1442

Query: 1180 ccatcaagattgcaccacccgaaacacctgactccaaagttcgatgggttatcatcactg 1239
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Sbjct: 1443 ccatcaagattgctccaccagaaacacctgactccaaagttcgaatgggtcgatcactg 1502

Query: 1240 gaccgccagaggcccaattcaaggctcaggggaagaatctatggcaaactcaaggaggaga 1299
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Sbjct: 1503 gacccccagaggctcagttcaaggctcaggggaagaatttatggcaaactaaaagaagaga 1562

Query: 1300 acttctttggtcccaaggaggaagtgaagctggagaccacatacgtgtgccagcatcag 1359
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Sbjct: 1563 atttctttggtcccaaggaggaagtaaagctagagaccacatacgggttcgggttcag 1622

Query: 1360 cagctggccgggtcattggcaaagggtggaaaaacgggtgaacgagttgcagaatttgacgg 1419
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Sbjct: 1623 cagccggccgcgtcatcggcaaaggcggcaaaacgggtgaatgagctgcagaacttgactg 1682

Query: 1420 cagctgaggtggtagtaccaagagaccagacccctgatgagaacgaccaggtcatcgtga 1479
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Sbjct: 1683 cagctgaggtggtagtgccaagagaccagaccccgatgagaacgaccaagtcattgtta 1742

Query: 1480 aaatcatcggacatttctatgccagtcagatgggtcaacggaagatccgagacatcctgg 1539
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Sbjct: 1743 agatcatcggacatttttatgccagccagatgggtcagcggaagatccgagacatcctgg 1802

Query: 1540 cccagggttaagcagcagcatcagaagggacagagtaaccaggcccaggcacggaggaagt 1599
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Sbjct: 1803 ctcaagtttaagcaacagcaccagaagggacagagcaacctggcccaggctcggaggaagt 1862

Query: 1600 gacca-gcccc-tccctgtccc 1619
|||||

Sbjct: 1863 gacccccgccccctcc-tgtccc 1883

>gi|31560605|ref|NM_009951.2| Mus musculus insulin-like growth factor 2, binding pro
(Igf2bp1), mRNA
Length = 2780

Score = 1886 bits (981), Expect = 0.0
Identities = 1343/1521 (88%), Gaps = 11/1521 (0%)
Strand = Plus / Plus

Query: 108 agggagccggaaaaattcaaatccgaaatattccacccagctccgatgggaagtactggac 167
Sbjct: 513 agggatcggaataacagattcgcaatattccacctcagctccgatgggaagtgcctagat 572

Query: 168 agcctgctgggtcagtatggtacagtagagaactgtgagcaagtgaacaccgagagtgcag 227
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Query: 228 acggcagtggtgaatgtcacctattccaaccgggagcagaccaggcaagccatcatgaag 287
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Query: 288 ctgaatggccaccagttggagaaccatgccctgaaggctcctacatccccgatgagcag 347
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Query: 348 atagcacagggacctgagaatgggcgcagggggctttgggtctcggggctcagcccc-g 406
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Query: 407 ccagggctcacctgtggcagcgggggccccagccaagcagcagcaagtggacatccccct 466
Sbjct: 813 caaggg-tcgcccggtggcagcaggggctccagccaagcagcagccagtggacatccctct 871

Query: 467 tcgggtcctggtgcccaccagtatgtgggtgccattattggcaaggagggggccaccat 526
Sbjct: 872 ccgggtcctggtgcctacgcagtatgtaggcgctatcattggcaaggaggggtgccaccat 931

Query: 527 ccgcaacatcacaaaacagacccagtcgaagatagacgtgcataggaaggagaacgcagg 586
Sbjct: 932 ccgaaacatcacaaaacagacgcagtcgaagatagacgtgcataggaaggagaatgcggg 991

Query: 587 tgcagctgaaaaagccatcagtggtgcactccaccctgagggtgctcctccgcttgtaa 646
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Query: 647 gatgatcttgagattatgcataaaggaggtgaaggacacccaaacggctgacgaggttcc 706
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Query: 707 cctgaagatcctggcccataataactttgtagggcgctctcattggcaaggaaggacggaa 766
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Query: 767 cctgaagaaggtagagcaagataccgagacaaaaatcaccatctcctcggttgcaagacct 826
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Query: 827 taccctttacaaccctgagaggaccatcactgtgaagggggccatcgagaattggtgcag 886
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Query: 887 ggccgagcaggaaataatgaagaaagttcgggaggcctatgagaatgatgtggctgccat 946
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Query: 1121 cgccatcatcggaagaaggggagcagcatcaaagctctcccggtttgccagcgcctc 1180
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Query: 1241 accgccagaggcccaattcaaggctcaggggaagaatctatggcaaactcaaggaggagaa 1300
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Query: 1301 cttctttggtcccaaggaggaagtgaagctggagacccacatacgtgtgccagcatcagc 1360
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Query: 1361 agctggccgggtcatttggaaggtggaaaaacggtgaacgagttgcagaatttgacggc 1420
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Query: 1421 agctgaggtggttagtaccagagaccagacccctgatgagaacgaccaggtcatcgtgaa 1480
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Query: 1481 aatcatcggacatttctatgccagtcagatgggtcaacggaagatccgagacatcctggc 1540
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Sbjct: 1892 gatcatcggacatttctatgccagccagatgggtcagcggaagatccgagacatcctggc 1951

Query: 1541 ccagggttaagcagcagcatcagaagggacagagtaaccagggccaggcacggaggaagtg 1600
|||
Sbjct: 1952 tcaaggttaagcaacagcaccagaagggacagagcaacctggcccagggtcggaggaagtg 2011

Query: 1601 acca-gcccc-tccctgtccc 1619
|||
Sbjct: 2012 accccgccccctcc-tgtccc 2031

>gi|12851513|dbj|AK013940.1| Mus musculus 13 days embryo head cDNA, RIKEN full-length library, clone:3110001D23 product:insulin-like growth factor 2, binding protein 1, full insert sequence
Length = 2780

Score = 1886 bits (981), Expect = 0.0
Identities = 1343/1521 (88%), Gaps = 11/1521 (0%)
Strand = Plus / Plus

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Query: 108  aggagccggaataattcaaatccgaaatattccaccccagctccgatgggaagtactggac 167
          ||||| ||||| || || || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 513  aggagtcggaataacagattcgcaatattccacctcagctccgatgggaagtgctagat 572

Query: 168  agcctgctgggtcagtatggtacagtagagaactgtgagcaagtgaacaccgagagtga 227
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 573  agcctgctgggtcagtacggtacagtggagaactgtgagcaagtgaacactgaaagtga 632

Query: 228  acggcagtggtgaatgtcacctattccaaccgggagcagaccaggcaagccatcatgaag 287
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Sbjct: 633  acagctgtggtcaacgtcacctactctaaccgggagcagaccaggcaagctatcatgaag 692

Query: 288  ctgaatggccaccagttggagaacctatgcctgaaggtctcctacatccccgatgagcag 347
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Sbjct: 693  ctaaatggccatcaactggagaacctatgcctgaaggtctcctacatacctgatgagcag 752

Query: 348  atagcacaggacctgagaatgggcgcgagggggctttggctctcggggtcagcccc-g 406
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Sbjct: 753  ataacgcaaggctcctgagaatgggcgctcgtggaggctttgggtctcggggccagccccg 812

Query: 407  ccagggctcacctgtggcagcgggggccccagccaagcagcagcaagtggacatccccct 466
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Sbjct: 813  caaggg-tcgcccgtggcagcaggggctccagccaagcagcagccagtggacatccctct 871

Query: 467  tcggctcctgggtgccaccagtatgtgggtgccattattggcaaggagggggccaccat 526
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Sbjct: 872  ccggctcctgggtgcctacgcagtatgtaggcgctatcattggcaaggaggggtgccaccat 931

Query: 527  ccgcaacatcacaaaacagaccagtcgaagatagacgtgcataggaaggagaacgcagg 586
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Sbjct: 932  ccgaaacatcacaaaacagacgcagtcgaagatagacgtgcataggaaggagaatgcggg 991

Query: 587  tgcagctgaaaaagccatcagtgctcactccaccctgagggtgctcctccgcttgtaa 646
          || || || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Query: 647  gatgatcttgagattatgcataaagaggctaaggacacaaaaacggctgacgaggttcc 706
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Sbjct: 1052 gatgatcttgagattatgcacaaggaggcaaaggacacaaaaacggcagatgaagttcc 1111

Query: 707  cctgaagatcctggcccataataactttgtagggcgtctcattggcaaggaaggacggaa 766
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Sbjct: 1112 cctgaagatcctggctcataacaacttcgtcgggcgactcattggcaaggaaggcgaa 1171
```



Your request has been successfully submitted and put into the Blast Queue.

Query = (3412 letters)

seq 4
translated \Rightarrow translated db
[blast x]

The request ID is 1061911575-20294-2284897.BLASTQ3

Format! or **Reset all**

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ Linkout ☐ Sequence Retrieval ☒ NCBI-gi Alignment in HTML

Number of: Descriptions 100 Alignments 50

Alignment view Pairwise

Limit results by
entrez query or select from: (none)

Expect value
range:

megablast SEQ ID NO: 6



Your request has been successfully submitted and put into the Blast Queue.

Query = (3412 letters)

The request ID is

or

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi in

Number of: Descriptions Alignments

Alignment view

Start formatting
from query #

Limit results by or select from:

Expect value
range:

Results file ☐



results of BLAST

BLASTN 2.2.6 [Apr-09-2003]

RID: 1061911546-21269-1691103.BLASTQ3

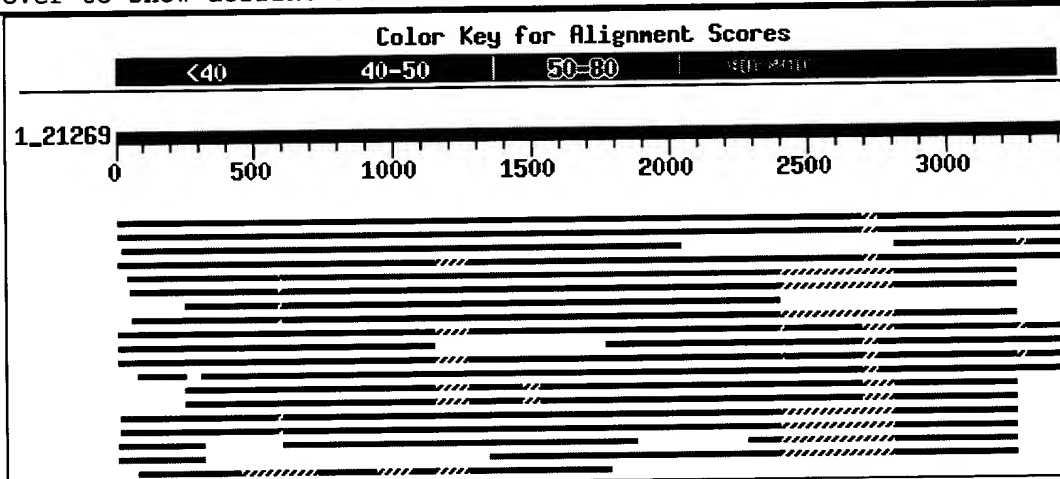
Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)
1,886,208 sequences; 8,918,056,233 total letters

Taxonomy reports

Query=
(3412 letters)

Distribution of 80 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score E
(bits) Value

gi	27552765	ref	NM_006548.2	Homo sapiens IGF-II mRNA-bindin...	5107	0.0
gi	33878041	gb	BC021290.2	Homo sapiens IGF-II mRNA-binding...	5105	0.0
gi	4191609	gb	AF117107.1	AF117107 Homo sapiens IGF-II mRNA...	3826	0.0
gi	4883680	gb	AF057352.1	AF057352 Homo sapiens hepatocellul...	2675	0.0
gi	23958572	gb	BC023758.1	Mus musculus RIKEN cDNA C330012H...	2182	0.0
gi	26093366	dbj	AK049196.1	Mus musculus ES cells cDNA, RIK...	2182	0.0
gi	26090647	dbj	AK044984.1	Mus musculus 9.5 days embryo pa...	2177	0.0
gi	26097330	dbj	AK077404.1	Mus musculus 6 days neonate hea...	2165	0.0
gi	7656675	gb	AC020629.6	Homo sapiens 12q BAC RP11-76E16 (...)	1873	0.0
gi	27485839	ref	XM_208686.1	Homo sapiens similar to hepato...	1865	0.0
gi	15552942	emb	AL596177.4	Human DNA sequence from clone R...	1759	0.0
gi	27413166	gb	AC016961.28	Homo sapiens 3 BAC RP11-394J21 ...	1708	0.0
gi	31873661	emb	BX537583.1	HSM806243 Homo sapiens mRNA; cDN...	1708	0.0
gi	19849375	gb	AC104980.5	Homo sapiens chromosome 8, clone...	1665	0.0
gi	17298202	dbj	AP004290.2	Homo sapiens genomic DNA, chrom...	1659	0.0
gi	33942111	ref	NM_183029.1	Mus musculus RIKEN cDNA C33001...	1240	0.0
gi	32451876	gb	BC054552.1	Mus musculus cDNA clone MGC:6242...	1240	0.0

gi	27666189	ref	XM 221343.1	Rattus norvegicus similar to I...	1221	0.0
gi	28492961	ref	XM 193835.2	Mus musculus RIKEN cDNA C33001...	1175	0.0
gi	30148117	ref	XM 291469.2	Homo sapiens similar to hepato...	827	0.0
gi	18464262	gb	AC105413.3	Homo sapiens BAC clone RP11-64A1...	669	0.0
gi	23355671	gb	AC108670.10	Homo sapiens 3 BAC RP11-218A22 ...	479	e-131
gi	17737024	gb	AC009247.13	AC009247 Homo sapiens 3q27 BAC ...	479	e-131
gi	26082515	dbj	AK031773.1	Mus musculus 11 days embryo hea...	406	e-109
gi	27665993	ref	XM 221344.1	Rattus norvegicus similar to I...	302	3e-78

Alignments

>gi|27552765|ref|NM_006548.2| Homo sapiens IGF-II mRNA-binding protein 2 (IMP-2), mR
Length = 3642

Score = 5107 bits (2656), Expect = 0.0

Identities = 2671/2686 (99%)

Strand = Plus / Plus

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Query: 65     gacggatgatgaacaagctttacatcggaacctgagccccgccgtcaccgccgacgacc 124
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Sbjct: 189    gctacgccttcgtggactaccccgaccagaactgggccatccgcgccatcgagaccctct 248

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Query: 305    taaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtgggaggtgttgg 364
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Sbjct: 309    taaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtgggaggtgttgg 368

Query: 365    atggacttttggtcaatatgggacagtggagaatgtggaacaagtcaacacagacacag 424
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Sbjct: 369    atggacttttggtcaatatgggacagtggagaatgtggaacaagtcaacacagacacag 428

Query: 425    aaaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaatagccatggaga 484
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Sbjct: 429    aaaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaatagccatggaga 488

Query: 485    agctaagcgggcatcagtttgagaactactccttcaagatttcctacatcccggatgaag 544
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Query: 545    aggtgagctccccttcgccccctcagcgagcccagcggtggggaccactcttccgggagc 604

```


Sbjct: 549 |||||
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Query: 605 aagggcacgcccctgggggcacttctcaggccagacagattgatttcccgctgcggatcc 664
|||||

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|||||

Sbjct: 669 tgggtccccaccagtttgttgggtgccatcatcggaaggagggttgaccataaagaaca 728

Query: 725 tcactaagcagaccagtcgccggtagatatccatagaaaagagaactctggagctgcag 784
|||||

Sbjct: 729 tcactaagcagaccagtcgccggtagatatccatagaaaagagaactctggagctgcag 788

Query: 785 agaagcctgtcaccatccatgccaccccagaggggacttctgaagcatgccgcatgattc 844
|||||

Sbjct: 789 agaagcctgtcaccatccatgccaccccagaggggacttctgaagcatgccgcatgattc 848

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|||||

Sbjct: 1149 aagccaatctgatcccagggttgaacctcagcgcaacttggcatcttttaacaggactgt 1208

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Query: 1265 tcactaccactccggatacttctccagcctgtacccccatcaccagtttgcccgttcc 1324
|||||

Sbjct: 1269 tcactaccactccggatacttctccagcctgtacccccatcaccagtttgcccgttcc 1328

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Query: 1385 tgggcgccatcatcggaagaagggggcacacatcaaacagctggcgagattcgccggag 1444
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Query: 1565 aaaacttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgcctctt 1624
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Sbjct: 1569 aaaacttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgcctctt 1628
|||||

Query: 1625 ccacagctggccgggtgattggcaaaggtggcaagaccgtgaacgaactgcagaacttaa 1684
|||||

Sbjct: 1629 ccacagctggccgggtgattggcaaaggtggcaagaccgtgaacgaactgcagaacttaa 1688
|||||

Query: 1685 ccagtgcagaagtcacgtgcctcgtgaccaaaccgagatgaaaatgaggaagtgatcg 1744
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Sbjct: 1689 ccagtgcagaagtcacgtgcctcgtgaccaaaccgagatgaaaatgaggaagtgatcg 1748
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Query: 1745 tcagaattatcgggcacttctttgctagccagactgcacagcgcaagatcagggaaattg 1804
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Sbjct: 1749 tcagaattatcgggcacttctttgctagccagactgcacagcgcaagatcagggaaattg 1808
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Query: 1805 tacaacaggtgaagcagcaggagcagaaataccctcagggagtcgcctcacagcgagca 1864
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Sbjct: 1809 tacaacaggtgaagcagcaggagcagaaataccctcagggagtcgcctcacagcgagca 1868
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Query: 1865 agtgaggctcccacaggcaccagcaaaacaacggatgaatgtagcccttccaacacctga 1924
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Sbjct: 1869 agtgaggctcccacaggcaccagcaaaacaacggatgaatgtagcccttccaacacctga 1928
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Query: 1925 cagaatgagaccaaaccgcagccagccagatcgggagcaaaccaaagaccatctgaggaat 1984
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Sbjct: 1929 cagaatgagaccaaaccgcagccagccagatcgggagcaaaccaaagaccatctgaggaat 1988
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Query: 1985 gagaagtctgcggaggcgccagggactctgccgaggccctgagaacccaggggccgag 2044
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Sbjct: 1989 gagaagtctgcggaggcgccagggactctgccgaggccctgagaacccaggggccgag 2048
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Query: 2045 gaggggccccggaaggtcagccaggtttgccagaaccaccgagccccgcctcccgcccccc 2104
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Sbjct: 2049 gaggggccccggaaggtcagccaggtttgccagaaccaccgagccccgcctcccgcccccc 2108
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Query: 2105 agggcttctgcaggcttcagccatccacttcacatccactcgatctctcctgaactcc 2164

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Sbjct: 2109 agggcttctgcaggcttcagccatccacttcaccatccactcggatctctcctgaactcc 2168

Query: 2165 caccgacgctatcccttttagttgaactaacataggtgaacgtgttcaaagccaagcaaaa 2224
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Sbjct: 2169 caccgacgctatcccttttagttgaactaacataggtgaacgtgttcaaagccaagcaaaa 2228

Query: 2225 tgcacaccctttttctgtggcaaactcgtctctgtacatgtgtgtacatattagaaagggga 2284
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Query: 2285 agatgttaagatatgtggcctgtgggttacacaggggtgcctgcagcggtaatatatttta 2344
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Sbjct: 2289 agatgttaagatatgtggcctgtgggttacacaggggtgcctgcagcggtaatatatttta 2348

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Query: 2405 nnnnnnnnaagagaaagcaggcttttctagactttaagaataaagtctttgggaggtct 2464
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Sbjct: 2529 tcggaaggacactcacggcagttctggatcacctgtgtatgtcaacagaagggataccgt 2588

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Score = 1058 bits (550), Expect = 0.0
Identities = 609/665 (91%), Gaps = 2/665 (0%)
Strand = Plus / Plus

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Query: 2809 nnaggcaaagcagtgtctgtgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 2868
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Sbjct: 2813 c-aggcaaagcagtgtctgtgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 2871

Query: 2869 aaccagcctcaacttacacttggttactcaaaagaacaagagtcaatgggtacttgtccta 2928
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Sbjct: 2872 aaccagcctcaacttacacttggttactcaaaagaacaagagtcaatggtacttgtccta 2931

Query: 2929 gcgttttggagaggaaaacaggaacccaccaaaccaaatcaaccaaacaagaaaa 2988
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Sbjct: 2932 gcgttttggagaggaaaacaggaacccaccaaaccaaatcaaccaaacaagaaaa 2991

Query: 2989 aattccacaatgaaagaatgtattttgtctttttgcattttggtgtataagccatcaata 3048
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2992 aattccacaatgaaagaatgtattttgtctttttgcattttggtgtataagccatcaata 3051

Query: 3049 ttcagcaaaatgattcctttctttnnnnnnnnnnn-tgtggaggaaagtagaaatttacc 3107
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Sbjct: 3052 ttcagcaaaatgattcctttcttttaaaaaaaaaaagtgtggaggaaagtagaaatttacc 3111

Query: 3108 aaggttggtggcccgaggcggttaaatcacagannnnnnnaacgagaaaaacacacagaa 3167
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Sbjct: 3112 aaggttggtggcccgaggcggttaaatcacagatttttttaacgagaaaaacacacagaa 3171

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Sbjct: 3172 gaagctacctcaggtgtttttacctcagcaccttgccttctgtgtttcccttagagatttt 3231

Query: 3228 gtaaagctgatagttggagcannnnnnnnnnnnnnnaataaaaaatgagttggnnnnnnnn 3287
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3232 gtaaagctgatagttggagcatttttttatttttttaataaaaaatgagttggaaaaaaa 3291

Query: 3288 taagatatcaactgccagcctggagaaggtgacagtccaagtgtgcaacagctgttctga 3347
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3292 taagatatcaactgccagcctggagaaggtgacagtccaagtgtgcaacagctgttctga 3351

Query: 3348 attgtcttcgctagccaagaacnataatggccttcttttggacaaaccttgaaaatggt 3407
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Sbjct: 3352 attgtcttcgctagccaagaacnataatggccttcttttggacaaaccttgaaaatggt 3411

Query: 3408 tatttt 3412
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Sbjct: 3412 tatttt 3416
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>gi|33878041|gb|BC021290.2| Homo sapiens IGF-II mRNA-binding protein 2, mRNA (cDNA c
MGC:29539 IMAGE:5090334), complete cds
Length = 3633

Score = 5105 bits (2655), Expect = 0.0
Identities = 2670/2685 (99%)
Strand = Plus / Plus

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Query: 6      cggaggaggcgaggagcgccgggtaccgggcccgggggagccgcgggctctcggggaagag 65
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1      cggaggaggcgaggagcgccgggtaccgggcccgggggagccgcgggctctcggggaagag 60

Query: 66     acggatgatgaacaagctttacatcgggaaacctgagccccgccgtcaccgccgacgacct 125
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61     acggatgatgaacaagctttacatcgggaaacctgagccccgccgtcaccgccgacgacct 120
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Query: 126	ccggcagctctttggggacaggaagctgccctggcgggacaggtcctgctgaagtcgg	185
Sbjct: 121	ccggcagctctttggggacaggaagctgccctggcgggacaggtcctgctgaagtcgg	180
Query: 186	ctacgccttcgtggactaccccgaccagaactgggccatccgcgccatcgagaccctctc	245
Sbjct: 181	ctacgccttcgtggactaccccgaccagaactgggccatccgcgccatcgagaccctctc	240
Query: 246	gggtaaagtgggaattgcatgggaaaatcatggaagttgattactcagtctctaaaaagct	305
Sbjct: 241	gggtaaagtgggaattgcatgggaaaatcatggaagttgattactcagtctctaaaaagct	300
Query: 306	aaggagcagggaaaattcagattcgaaacatccctcctcacctgcagtgagggtgttgga	365
Sbjct: 301	aaggagcagggaaaattcagattcgaaacatccctcctcacctgcagtgagggtgttgga	360
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Sbjct: 361	tggacttttggtcaatatgggacagtgaggaaatgtggaacaagtcaacacagacacaga	420
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Sbjct: 421	aaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaatagccatggagaa	480
Query: 486	gctaagcgggcatcagtttgagaactactccttcaagatttcctacatcccggatgaaga	545
Sbjct: 481	gctaagcgggcatcagtttgagaactactccttcaagatttcctacatcccggatgaaga	540
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Sbjct: 541	ggtgagctccccttcgccccctcagcgagcccagcgtggggaccactcttcccgggagca	600
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Sbjct: 601	aggccacgcccctgggggcacttctcaggccagacagattgatttcccgctgcggatcct	660
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Sbjct: 661	ggtccccaccagtttggttggtgccatcatcggaaggagggttgaccataaagaacat	720
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Sbjct: 721	cactaagcagaccagtcgggtagatatccatagaaaagagaactctggagctgcaga	780
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Sbjct: 781	gaagcctgtcaccatccatgccaccccagaggggacttctgaagcatgccgcatgattct	840
Query: 846	tgaaatcatgcagaaagaggcagatgagaccaaaactagccgaagagattcctctgaaaat	905
Sbjct: 841	tgaaatcatgcagaaagaggcagatgagaccaaaactagccgaagagattcctctgaaaat	900

Query: 906 cttggcacacaatggcttggttgaagactgattggaaaagaaggcagaaatttgaagaa 965
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Sbjct: 901 cttggcacacaatggcttggttgaagactgattggaaaagaaggcagaaatttgaagaa 960

Query: 966 aattgaacatgaaacagggaccaagataacaatctcatctttgcaggatttgagcatata 1025
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Sbjct: 961 aattgaacatgaaacagggaccaagataacaatctcatctttgcaggatttgagcatata 1020

Query: 1026 caaccggaagaaccatcactgtgaagggcacagttgaggcctgtgccagtgtgagat 1085
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Query: 1086 agagattatgaagaagctgcgtgaggcctttgaaaatgatatgctggctgttaaccaaca 1145
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Query: 1146 agccaatctgatcccaggggtgaacctcagcgcacttggcatcttttcaacaggactgtc 1205
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Sbjct: 1381 gggcgccatcatcggaagaagggggcacacatcaaacagctggcgagattcgccggagc 1440

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Sbjct: 1681 cagtgcagaagtcatcgtgcctcgtgaccaaaccgagatgaaaatgaggaagtgatcgt 1740

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Sbjct: 1801 acaacaggtgaagcagcaggagcagaaataccctcaggagtcgcctcacagcgagcaa 1860

Query: 1866 gtgaggctccacaggcaccagcaaaacaacggatgaatgtagcccttccaacacctgac 1925
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Sbjct: 1861 gtgaggctccacaggcaccagcaaaacaacggatgaatgtagcccttccaacacctgac 1920

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Query: 1986 agaagtctgcggaggcggccagggactctgccgaggccctgagaaccccaggggcccagg 2045
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Sbjct: 2221 gcacacccttttctgtggcaaatcgtctctgtacatgtgtgtacatattagaaaggaa 2280

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Query: 2646 ttgcttcacaggttttaaaactggttttttgcatactgctatataa 2690
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Score = 1058 bits (550), Expect = 0.0
Identities = 609/665 (91%), Gaps = 2/665 (0%)
Strand = Plus / Plus

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Sbjct: 3343 attgtcttccgctagccaagaacctatatggccttcttttggacaaaccttgaaaatgtt 3402

Query: 3408 tattt 3412
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Sbjct: 3403 tattt 3407

>gi|4191609|gb|AF117107.1|AF117107 Homo sapiens IGF-II mRNA-binding protein 2 (IMP-2)
Length = 2010

Score = 3826 bits (1990), Expect = 0.0
Identities = 2007/2014 (99%), Gaps = 6/2014 (0%)
Strand = Plus / Plus

Query: 22 cgccgggtaccgggccc-ggggagccgcccgtctc-ggggaagagacggatgatgaaca 79
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Sbjct: 1 cgccgggtacc--gccgtagggagccgc-ggc-ctcaggggaagagacggatgatgaaca 56

Query: 80 agctttacatcgggaaacctgagccccgccgtcaccgccgacgacctccggcagctctttg 139
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Sbjct: 57 agctttacatcgggaaacctgagccccgccgtcaccgccgacgacctccggcagctctttg 116

Query: 140 gggacaggaagctgcccctggcgggacaggtcctgctgaagtccggctacgccttcgtgg 199
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Sbjct: 117 gggacaggaagctgcccctggcgggacaggtcctgctgaagtccggctacgccttcgtgg 176

Query: 200 actaccccgaccagaactgggccatccgcgccatcgagaccctctcgggtaaagtggaat 259
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Sbjct: 177 actaccccgaccagaactgggccatccgcgccatcgagaccctctcgggtaaagtggaat 236

Query: 260 tgcattgggaaaatcatggaagttgattactcagtctctaaaaagctaaggagcaggaaaa 319
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Sbjct: 237 tgcattgggaaaatcatggaagttgattactcagtctctaaaaagctaaggagcaggaaaa 296

Query: 320 ttcagattcgaaacatccctcctcacctgcagtgggaggtgttgatggacttttggctc 379
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Sbjct: 297 ttcagattcgaaacatccctcctcacctgcagtgggaggtgttgatggacttttggctc 356

Query: 380 aatatgggacagtggagaatgtggaacaagtcaacacagacacagaaaccgccgttgtca 439
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Sbjct: 357 aatatgggacagtggagaatgtggaacaagtcaacacagacacagaaaccgccgttgtca 416

Query: 440 acgtcacatatgcaacaagagaagaagcaaaaatagccatggagaagctaagcgggcatc 499

Sbjct: 417 |||||
acgtcacatatgcaacaagagaagaagcaaaaatagccatggagaagctaagcgggcatc 476

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|||||

Sbjct: 477 agtttgagaactactccttcaagatttctacatcccggatgaagaggtgagctcccctt 536
|||||

Query: 560 cgccccctcagcgagcccagcgtggggaccactcttcccgggagcaaggccacgccccctg 619
|||||

Sbjct: 537 cgccccctcagcgagcccagcgtggggaccactcttcccgggagcaaggccacgccccctg 596
|||||

Query: 620 ggggcacttctcaggccagacagattgatttcccgctgcggatcctggtccccaccagt 679
|||||

Sbjct: 597 ggggcacttctcaggccagacagattgatttcccgctgcggatcctggtccccaccagt 656
|||||

Query: 680 ttgttggtgccatcatcggaaggagggttgaccataaagaacatcactaagcagaccc 739
|||||

Sbjct: 657 ttgttggtgccatcatcggaaggagggttgaccataaagaacatcactaagcagaccc 716
|||||

Query: 740 agtcccgggtagatatccatagaaaagagaactctggagctgcagagaagcctgtcacca 799
|||||

Sbjct: 717 agtcccgggtagatatccatagaaaagagaactctggagctgcagagaagcctgtcacca 776
|||||

Query: 800 tccatgccaccccagaggggacttctgaagcatgccgcatgattcttgaaatcatgcaga 859
|||||

Sbjct: 777 tccatgccaccccagaggggacttctgaagcatgccgcatgattcttgaaatcatgcaga 836
|||||

Query: 860 aagaggcagatgagaccaaactagccgaagagattcctctgaaaatcttggcacacaatg 919
|||||

Sbjct: 837 aagaggcagatgagaccaaactagccgaagagattcctctgaaaatcttggcacacaatg 896
|||||

Query: 920 gcttggttgaagactgattggaaaagaaggcagaaatttgaagaaaattgaacatgaaa 979
|||||

Sbjct: 897 gcttggttgaagactgattggaaaagaaggcagaaatttgaagaaaattgaacatgaaa 956
|||||

Query: 980 cagggaccaagataacaatctcatctttgcaggatttgagcatatacaacccggaaagaa 1039
|||||

Sbjct: 957 cagggaccaagataacaatctcatctttgcaggatttgagcatatacaacccggaaagaa 1016
|||||

Query: 1040 ccatcactgtgaagggcacagttgaggcctgtgccagtgtgagatagagattatgaaga 1099
|||||

Sbjct: 1017 ccatcactgtgaagggcacagttgaggcctgtgccagtgtgagatagagattatgaaga 1076
|||||

Query: 1100 agctgcgtgaggcctttgaaaatgatatgctggctgttaaccaacaagccaatctgatcc 1159
|||||

Sbjct: 1077 agctgcgtgaggcctttgaaaatgatatgctggctgttaaccaacaagccaatctgatcc 1136
|||||

Query: 1160 cagggttgaacctcagcgcacttggcatcttttcaacaggactgtccgtgctatctccac 1219
|||||

Sbjct: 1137 cagggttgaacctcagcgcacttggcatcttttcaacaggactgtccgtgctatctccac 1196
|||||

Query: 1220 cagcagggccccgcggagctccccccgctgccccctaccaccccttactaccactccg 1279

Sbjct: 1197 |||||cagcagggccccgcggagctccccccgctgccccctaccacccttcactaccactccg 1256

Query: 1280 gatacttctccagcctgtacccccatcaccagtttgccccgttcccgcacatcactctt 1339
|||||

Sbjct: 1257 gatacttctccagcctgtacccccatcaccagtttgccccgttcccgcacatcactctt 1316

Query: 1340 atccagagcaggagattgtgaatctcttcacccaacccaggctgtggcgccatcatcg 1399
|||||

Sbjct: 1317 atccagagcaggagattgtgaatctcttcacccaacccaggctgtggcgccatcatcg 1376

Query: 1400 ggaagaagggggcacacatcaaacagctggcgagattcgccggagcctctatcaagattg 1459
|||||

Sbjct: 1377 ggaagaagggggcacacatcaaacagctggcgagattcgccggagcctctatcaagattg 1436

Query: 1460 cccctgcggaaggccagacgtcagcgaaaggatggatcatcatcaccgggccaccggaag 1519
|||||

Sbjct: 1437 cccctgcggaaggccagacgtcagcgaaaggatggatcatcatcaccgggccaccggaag 1496

Query: 1520 cccagttcaaggcccagggacggatctttgggaaactgaaagaggaaaacttctttaacc 1579
|||||

Sbjct: 1497 cccagttcaaggcccagggacggatctttgggaaactgaaagaggaaaacttctttaacc 1556

Query: 1580 ccaaagaagaagtgaagctggaagcgcatatcagagtgcctcttcacagctggccggg 1639
|||||

Sbjct: 1557 ccaaagaagaagtgaagctggaagcgcatatcagagtgcctcttcacagctggccggg 1616

Query: 1640 tgattggcaaaggtggcaagaccgtgaacgaactgcagaacttaaccagtgcagaagtca 1699
|||||

Sbjct: 1617 tgattggcaaaggtggcaagaccgtgaacgaactgcagaacttaaccagtgcagaagtca 1676

Query: 1700 tcgtgcctcgtgaccaaacgccagatgaaaatgaggaagtgatcgtcagaattatcgggc 1759
|||||

Sbjct: 1677 tcgtgcctcgtgaccaaacgccagatgaaaatgaggaagtgatcgtcagaattatcgggc 1736

Query: 1760 acttctttgctagccagactgcacagcgcaagatcagggaaattgtacaacaggtgaagc 1819
|||||

Sbjct: 1737 acttctttgctagccagactgcacagcgcaagatcagggaaattgtacaacaggtgaagc 1796

Query: 1820 agcaggagcagaaataccctcagggagtcgcctcacagcgcagcaagtgaggctcccaca 1879
|||||

Sbjct: 1797 agcaggagcagaaataccctcagggagtcgcctcacagcgcagcaagtgaggctcccaca 1856

Query: 1880 ggcaccagcaaaaacaacggatgaatgtagccctccaacacctgacagaatgagacaaa 1939
|||||

Sbjct: 1857 ggcaccagcaaaaacaacggatgaatgtagccctccaacacctgacagaatgagacaaa 1916

Query: 1940 cgcagccagccagatcgggagcaaaccaaagaccatctgaggaatgagaagtctgcggag 1999
|||||

Sbjct: 1917 cgcagccagccagatcgggagcaaaccaaagaccatctgaggaatgagaagtctgcggag 1976

Query: 2000 gcggccagggactctgccgaggccctgagaaccc 2033

|||||
Sbjct: 1977 gcggccagggactctgccgaggccctgagaaccc 2010

>gi|4883680|gb|AF057352.1|AF057352 Homo sapiens hepatocellular carcinoma autoantigen
complete cds
Length = 3667

Score = 2675 bits (1391), Expect = 0.0
Identities = 1406/1421 (98%)
Strand = Plus / Plus

Query: 1270 acccactccggatacttctccagcctgtacccccatcaccagtttgccccgttcccgcat 1329
|||||
Sbjct: 1507 acccactccggatacttctccagcctgtacccccatcaccagtttgccccgttcccgcat 1566

Query: 1330 catcactcttatccagagcaggagattgtgaatctcttcatcccaaccaggctgtgggc 1389
|||||
Sbjct: 1567 catcactcttatccagagcaggagattgtgaatctcttcatcccaaccaggctgtgggc 1626

Query: 1390 gccatcatcgggaagaagggggcacacatcaaacagctggcgagattcgccggagcctct 1449
|||||
Sbjct: 1627 gccatcatcgggaagaagggggcacacatcaaacagctggcgagattcgccggagcctct 1686

Query: 1450 atcaagattgcccctgcggaaggcccagacgtcagcgaaaggatggatcatcatcaccggg 1509
|||||
Sbjct: 1687 atcaagattgcccctgcggaaggcccagacgtcagcgaaaggatggatcatcatcaccggg 1746

Query: 1510 ccaccggaagcccagttcaaggcccaggacggatctttgggaaactgaaagaggaaaac 1569
|||||
Sbjct: 1747 ccaccggaagcccagttcaaggcccaggacggatctttgggaaactgaaagaggaaaac 1806

Query: 1570 ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgcctcttccaca 1629
|||||
Sbjct: 1807 ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgcctcttccaca 1866

Query: 1630 gctggccgggtgattggcaaaggtggcaagaccgtgaacgaactgcagaacttaaccagt 1689
|||||
Sbjct: 1867 gctggccgggtgattggcaaaggtggcaagaccgtgaacgaactgcagaacttaaccagt 1926

Query: 1690 gcagaagtcacgtgcctcgtgaccaaacgccagatgaaaatgaggaagtgatcgtcaga 1749
|||||
Sbjct: 1927 gcagaagtcacgtgcctcgtgaccaaacgccagatgaaaatgaggaagtgatcgtcaga 1986

Query: 1750 attatcgggcacttctttgctagccagactgcacagcgcaagatcagggaaattgtacaa 1809
|||||
Sbjct: 1987 attatcgggcacttctttgctagccagactgcacagcgcaagatcagggaaattgtacaa 2046

Query: 1810 caggtgaagcagcaggagcagaaataccctcagggagtcgcctcacagcgagcaagtga 1869
|||||
Sbjct: 2047 caggtgaagcagcaggagcagaaataccctcagggagtcgcctcacagcgagcaagtga 2106

Query: 1870 ggctcccacaggcaccagcaaaaacaacggatgaatgtagcccttccaacacctgacagaa 1929
|||||
Sbjct: 2107 ggctcccacaggcaccagcaaaaacaacggatgaatgtagcccttccaacacctgacagaa 2166

Query: 1930 tgagaccaaacgcagccagccagatcgggagcaaaccaagaccatctgaggaatgagaa 1989
|||||
Sbjct: 2167 tgagaccaaacgcagccagccagatcgggagcaaaccaagaccatctgaggaatgagaa 2226

Query: 1990 gtctgcggaggcggccagggactctgccgaggccctgagaaccccaggggcccaggagggg 2049
|||||
Sbjct: 2227 gtctgcggaggcggccagggactctgccgaggccctgagaaccccaggggcccaggagggg 2286

Query: 2050 gcggggaaggtcagccaggtttgccagaaccaccgagccccgcctcccgccccccagggc 2109
|||||
Sbjct: 2287 gcggggaaggtcagccaggtttgccagaaccaccgagccccgcctcccgccccccagggc 2346

Query: 2110 ttctgcaggcttcagccatccacttcaccatccactcggatctctcctgaactcccacga 2169
|||||
Sbjct: 2347 ttctgcaggcttcagccatccacttcaccatccactcggatctctcctgaactcccacga 2406

Query: 2170 cgctatcccttttagttgaactaacataggtgaacgtgttcaaagccaagcaaaatgcac 2229
|||||
Sbjct: 2407 cgctatcccttttagttgaactaacataggtgaacgtgttcaaagccaagcaaaatgcac 2466

Query: 2230 accctttttctgtggcaaatcgtctctgtacatgtgtgtacatattagaaaggaagatg 2289
|||||
Sbjct: 2467 accctttttctgtggcaaatcgtctctgtacatgtgtgtacatattagaaaggaagatg 2526

Query: 2290 ttaagatatgtggcctgtgggttacacagggcgctgcagcggtaatatattttagaaat 2349
|||||
Sbjct: 2527 ttaagatatgtggcctgtgggttacacagggcgctgcagcggtaatatattttagaaat 2586

Query: 2350 aatatatcaaataactcaactaactccaatttttaataattattaannnnnnnnnnnnnn 2409
|||||
Sbjct: 2587 aatatatcaaataactcaactaactccaatttttaataattattaatttttttttcttt 2646

Query: 2410 nnaagagaaagcaggcttttctagactttaagaataaagtctttgggaggtctcacgg 2469
|||||
Sbjct: 2647 ttaagagaaagcaggcttttctagactttaagaataaagtctttgggaggtctcacgg 2706

Query: 2470 tgtagagaggagctttgaggccaccgcacaaaattcacccagagggaatctcgtcgga 2529
|||||
Sbjct: 2707 tgtagagaggagctttgaggccaccgcacaaaattcacccagagggaatctcgtcgga 2766

Query: 2530 aggacactcacggcagttctggatcacctgtgtatgtcaacagaagggaaccgtctcct 2589
|||||
Sbjct: 2767 aggacactcacggcagttctggatcacctgtgtatgtcaacagaagggaaccgtctcct 2826

Query: 2590 tgaagaggaaactctgtcactcctcatgcctgtctagctcatacaccatttctctttgc 2649
|||||
Sbjct: 2827 tgaagaggaaactctgtcactcctcatgcctgtctagctcatacaccatttctctttgc 2886

Query: 2650 ttcacaggttttaactgggtttttgcatactgctatataa 2690
|||||
Sbjct: 2887 ttcacaggttttaactgggtttttgcatactgctatataa 2927

Score = 2182 bits (1135), Expect = 0.0

Identities = 1135/1135 (100%)

Strand = Plus / Plus

```
Query: 6      cggaggaggcgaggagcgccgggtaccgggccgggggagccgcgggctctcggggaagag 65
             |||
Sbjct: 372    cggaggaggcgaggagcgccgggtaccgggccgggggagccgcgggctctcggggaagag 431

Query: 66     acggatgatgaacaagctttacatcggaacctgagccccgccgtcaccgccgacgacct 125
             |||
Sbjct: 432    acggatgatgaacaagctttacatcggaacctgagccccgccgtcaccgccgacgacct 491

Query: 126     ccggcagctctttggggacaggaagctgccctggcgggacaggtcctgctgaagtccgg 185
             |||
Sbjct: 492    ccggcagctctttggggacaggaagctgccctggcgggacaggtcctgctgaagtccgg 551

Query: 186     ctacgccttcgtggactaccccgaccagaactgggccatccgcgccatcgagaccctctc 245
             |||
Sbjct: 552    ctacgccttcgtggactaccccgaccagaactgggccatccgcgccatcgagaccctctc 611

Query: 246     gggtaaagtggaattgcatgggaaaatcatggaagttgattactcagtctctaaaaagct 305
             |||
Sbjct: 612    gggtaaagtggaattgcatgggaaaatcatggaagttgattactcagtctctaaaaagct 671

Query: 306     aaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtgggaggtgttgga 365
             |||
Sbjct: 672    aaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtgggaggtgttgga 731

Query: 366     tggacttttggctcaatatgggacagtggagaatgtggaacaagtcaacacagacacaga 425
             |||
Sbjct: 732    tggacttttggctcaatatgggacagtggagaatgtggaacaagtcaacacagacacaga 791

Query: 426     aaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaatagccatggagaa 485
             |||
Sbjct: 792    aaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaatagccatggagaa 851

Query: 486     gctaagcgggcatcagtttgagaactactccttcaagatttcctacatcccggatgaaga 545
             |||
Sbjct: 852    gctaagcgggcatcagtttgagaactactccttcaagatttcctacatcccggatgaaga 911

Query: 546     ggtgagctcccccttcgccccctcagcgagcccagcgtggggaccactcttcccgggagca 605
             |||
Sbjct: 912    ggtgagctcccccttcgccccctcagcgagcccagcgtggggaccactcttcccgggagca 971

Query: 606     aggccacgccccctgggggcacttctcaggccagacagattgatttcccgctgcggtatcct 665
             |||
Sbjct: 972    aggccacgccccctgggggcacttctcaggccagacagattgatttcccgctgcggtatcct 1031

Query: 666     ggtccccaccagtttggttggtgccatcatcggaaggagggttgaccataaagaacat 725
             |||
Sbjct: 1032   ggtccccaccagtttggttggtgccatcatcggaaggagggttgaccataaagaacat 1091
```

```
Query: 726 cactaagcagacccaggtcccgggtagatatccatagaaaagagaactctggagctgcaga 785
          |||
Sbjct: 1092 cactaagcagacccaggtcccgggtagatatccatagaaaagagaactctggagctgcaga 1151

Query: 786 gaagcctgtcaccatccatgccaccccagaggggacttctgaagcatgccgcatgattct 845
          |||
Sbjct: 1152 gaagcctgtcaccatccatgccaccccagaggggacttctgaagcatgccgcatgattct 1211

Query: 846 tgaaatcatgcagaaagaggcagatgagaccaaactagccgaagagattcctctgaaaat 905
          |||
Sbjct: 1212 tgaaatcatgcagaaagaggcagatgagaccaaactagccgaagagattcctctgaaaat 1271

Query: 906 cttggcacacaatggcttggttggaagactgattggaaaagaaggcagaaatttgaagaa 965
          |||
Sbjct: 1272 cttggcacacaatggcttggttggaagactgattggaaaagaaggcagaaatttgaagaa 1331

Query: 966 aattgaacatgaaacagggaccaagataacaatctcatctttgcaggatttgagcatata 1025
          |||
Sbjct: 1332 aattgaacatgaaacagggaccaagataacaatctcatctttgcaggatttgagcatata 1391

Query: 1026 caaccggaagaaccatcactgtgaagggcacagttgaggcctgtgccagtgtgagat 1085
          |||
Sbjct: 1392 caaccggaagaaccatcactgtgaagggcacagttgaggcctgtgccagtgtgagat 1451

Query: 1086 agagattatgaagaagctgcgtgaggcctttgaaaatgatatgctggctgttaac 1140
          |||
Sbjct: 1452 agagattatgaagaagctgcgtgaggcctttgaaaatgatatgctggctgttaac 1506

Score = 1052 bits (547), Expect = 0.0
Identities = 608/665 (91%), Gaps = 2/665 (0%)
Strand = Plus / Plus

Query: 2749 cattcttttgaatttcctcatccctccatctcaatcccgtatctacgcannnnnnnnnnn 2808
          |||
Sbjct: 2986 cattcttttgaatttcctcatccctccatctcaatcccgtatctacgca-ccccccccc 3044

Query: 2809 nnaggcaaagcagtgtctgtgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 2868
          |||
Sbjct: 3045 ccaggcaaagcagtgtctgtgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 3104

Query: 2869 aaccagcctcaacttacacttggttactcaaaagaacaagagtcaatgggtacttgtccta 2928
          |||
Sbjct: 3105 aaccagcctcaacttacacttggttactcaaaagaacaagagtcaatgggtacttgtccta 3164

Query: 2929 gcgtttttgaagaggaaaacaggaacccaccaaaccaaccaatcaaccaaacaagaaaa 2988
          |||
Sbjct: 3165 gcgtttttgaagaggaaaacaggaacccaccaaaccaaccaatcaaccaaacaagaaaa 3224

Query: 2989 aattccacaatgaaagaatgtattttgtctttttgcatttttggtgtataagccatcaata 3048
          |||
Sbjct: 3225 aattccacaatgaaagaatgtattttgtctttttgcatttttggtgtataagccatcaata 3284
```

Query: 3049 ttcagcaaaatgattcctttcttt-nnnnnnnnnntgtggaggaaagtagaaatttacc 3107
 |||||
 Sbjct: 3285 ttcagcaaaatgattcctttcttttaaaaaaaaaaagtgaggaaagtagaaatttacc 3344

Query: 3108 aagggtgttggtggccaggcggttaaattcacagannnnnnnaacgagaaaaacacacagaa 3167
 |||||
 Sbjct: 3345 aagggtgttggtggccaggcggttaaattcacagatttttttaacgagaaaaacacacagaa 3404

Query: 3168 gaagctacctcaggtgtttttacctcagcaccttgctcttggtttcccttagagatttt 3227
 |||||
 Sbjct: 3405 gaagctacctcaggtgtttttacctcagcaccttgatcttggtttcccttagagatttt 3464

Query: 3228 gtaaagctgatagttggagcannnnnnnnnnnnnaataaaaaatgagttggnnnnnnnn 3287
 |||||
 Sbjct: 3465 gtaaagctgatagttggagcatttttttatttttttaataaaaaatgagttggaaaaaaa 3524

Query: 3288 taagatatcaactgccagcctggagaagggtgacagtccaagtggtgcaacagctgttctga 3347
 |||||
 Sbjct: 3525 taagatatcaactgccagcctggagaagggtgacagtccaagtggtgcaacagctgttctga 3584

Query: 3348 attgtcttccgctagccaagaacnataatggccttcttttgacaaaccttgaaaatgtt 3407
 |||||
 Sbjct: 3585 attgtcttccgctagccaagaacctataatggccttcttttgacaaaccttgaaaatgtt 3644

Query: 3408 tattt 3412
 |||||
 Sbjct: 3645 tattt 3649

>gi|23958572|gb|BC023758.1| Mus musculus RIKEN cDNA C330012H03 gene, mRNA (cDNA clon
 IMAGE:5354659), partial cds
 Length = 3557

Score = 2182 bits (1135), Expect = 0.0
 Identities = 1607/1828 (87%), Gaps = 59/1828 (3%)
 Strand = Plus / Plus

Query: 596 cccgggagcaaggccac-gcccctgggggcatttctcaggccagacagattgatttcccg 654
 |||||
 Sbjct: 540 cccgggaacaaggccacggccc-gggagctcttctcaggccagacagattgatttcccg 598

Query: 655 ctgcggatcctggtccccaccagtttgttggtgccatcatcggaaggagggttgacc 714
 |||||
 Sbjct: 599 ctgcggatcctggtccccaccagtttgttggtgccatcatcggaaggagggttgacc 658

Query: 715 ataaagaacatcactaagcagaccagtcgggtagatatccatagaaaagagaactct 774
 |||||
 Sbjct: 659 ataaagaacatcactaagcagaccagtcgggtagacatccacagaaaggagaactct 718

Query: 775 ggagctgcagagaagcctgtcaccatccatgccacccagaggggacttctgaagcatgc 834
 |||||
 Sbjct: 719 ggggctgcagagaagcctgtcacatccatgctacccagaaggacatctgaagcatgc 778

Query: 835 cgcattgattcttgaaatcatgcagaaagaggcagatgagaccaaactagccgaagagatt 894
|||||
Sbjct: 779 cgcattgattcttgagattatgcaaaaagaagctgatgagaccaaactggctgaggagggt 838

Query: 895 cctctgaaaatcttggcacacaatggcttggttgaagactgattggaaaagaaggcaga 954
|||||
Sbjct: 839 cctctgaaaatcctggcccacaatggcttcggttgaagactgattggcaaagaaggcaga 898

Query: 955 aatttgaagaaaattgaacatgaaacagggaccaagataacaatctcatctttgcaggat 1014
|||
Sbjct: 899 aacctgaagaaaatagaacatgagacagggaccaagataaacatctcatccttgcaggat 958

Query: 1015 ttgagcatatacaacccggaaagaaccatcactgtgaagggca-cagttgaggcctgtgc 1073
|||||
Sbjct: 959 ttgagcatttataaccccgagagaaccatcacctgagggggcacca-ttgaagcctgtgc 1017

Query: 1074 cagtgtgagatagagattatgaagaagctgcgtgaggcctttgaaaatgatatgctggc 1133
|||
Sbjct: 1018 caatgtgtgagatagagattatgaagaagctccgagaggcctttgagaacgacatgctggc 1077

Query: 1134 tgtaaccaacaagccaatctgatcccagggttgaaacctcagcgacttggcatcttttc 1193
|||||
Sbjct: 1078 cgttaaccaacaagccaatctgatcccagggttaaacctcagtgacttggcatcttttc 1137

Query: 1194 aacaggactgtccgtgctat-ctccaccagcagggcccgaggagctcccccc-gctgcc 1251
|||
Sbjct: 1138 gactggactgtctgtgct-tcctccaccagcagggcccgaggagttccccccag-t-cc 1194

Query: 1252 -ccctaccacccttcaactaccactccggatacttctccagcctgtacccccatcacca 1310
|||||
Sbjct: 1195 tccctatcacccctttgctaccactccggatacttctccagctgtacccctcatcacca 1254

Query: 1311 gttt-ggcccgttcccgcatcatcactcttatccagagcaggagattgtgaa-tctcttc 1368
|||
Sbjct: 1255 -tttcggccattcccatcatcactcctaccagagcaggagactgt-aagtctcttc 1312

Query: 1369 atcccaaccaggctgtggcgccatcatcggaagaagggggcacacatcaaacagctg 1428
|||||
Sbjct: 1313 atcccaaccaggctgtgggtgctatcatcggaagaagggggcacacatcaaacagctc 1372

Query: 1429 gcgagattcgccggagcctctatcaagattgcccctgcggaaggcccagacgtcagcgaa 1488
|||
Sbjct: 1373 gctcgatttgctggtgcctccatcaagattgctccagcagaagggtccagatgtcagtgag 1432

Query: 1489 aggatggtcatcatcaccgggcccagggaagcccagttcaaggcccaggacggatcttt 1548
|||||
Sbjct: 1433 aggatggtcatcatcactgggtcctcctgaagcccagtttaagggtcaggacggatcttt 1492

Query: 1549 gggaaactgaaagaggaaaacttctttaaccccaaagaagaagtgaagctggaagcgcat 1608
|||||
Sbjct: 1493 gggaaactgaaggaagaaaacttctttaaccccaaagaagaagtgaagctggaggccac 1552

Query:	1609	atcacagagtgccttcttcacagctggccgpggtgattggcaaaggtaggaagaccgtgaac	1668
Sbjct:	1553	atccgagatcccctcgtcgaccgctggccgpggtgattggcaagggcgggaaaaccgtgaac	1612
Query:	1669	gaactgcagaacttaaccagtgcagaagtcatacgctgcctcgtgaccaaacgccagatgaa	1728
Sbjct:	1613	gagctgcagaacttgacaagtgagaagttatcgctgcctcgtgaccaaacgccagacgag	1672
Query:	1729	aatgaggaagtgatcgatcgatcagaattatcgggcacttctttgctagccagactgcacagcgc	1788
Sbjct:	1673	aatgaggaagtgatcgatcgatcagaattatcgggcatTTTTTTTgctagccagactgcacaacgc	1732
Query:	1789	aagatcagggaaattgtacaacaggtagaagcagcaggagcagaaaataacctcagggagtc	1848
Sbjct:	1733	aagatcagggaaattgtacagcaggtagaagcagcaggagcagagataacctcagggagtc	1792
Query:	1849	gcctcacagcgcagcaagtgaggctccccagggcaccagcaaaacaacggatgaatgtag	1908
Sbjct:	1793	gccccacagcgcagcaagtgaggctccccag-gaccagcaag-caaccgatgaatgtag	1850
Query:	1909	cccttccaacacctgacagaatgagacaaaacgcagccagccagatcgggagcaaaccaa	1968
Sbjct:	1851	ccctccaacacctgacaga-tgagacaaaac--agccagc-agatcggaagcaaaccaa	1906
Query:	1969	agaccatct-gaggaatgagaagtctgcggaggcggccagggactctgccgaggcc-ctg	2026
Sbjct:	1907	agagcatcccaggagtgatcgatctgcagag-cagccaggg-c-ctgcaga--cctct-	1960
Query:	2027	aga-accccagggg-ccgaggagggg-cggggaaggtagccagggttg-ccagaaccac	2082
Sbjct:	1961	acacatcct-gggatcc-aggagggcacagggaagg-c--c-aggtt-gtccagaaacac	2013
Query:	2083	cga--gccccgcctccc-gcc-ccccagggttctgcaggctt--cagccatccacttca	2136
Sbjct:	2014	cgcttggcctgcc-cccagcttcccctgg-cttctgcaggcataacagccatccactgc-	2070
Query:	2137	ccatcca-ctcggatctctcctgaactcccacgacgctatcccttttagttgaactaaca	2195
Sbjct:	2071	ccatccaactcagat-tctcctcagttcccaggacgctatccctttcggttgaactaaca	2129
Query:	2196	taggtgaacgtgttcaaagccaagcaaatgcac-acc-ttt-ttc-t-gtggcaaa-t	2249
Sbjct:	2130	taggtgaacatgctcaaagcaaaagcaaaattc-ctagccgttctttgttgtgg-aaagt	2187
Query:	2250	cgctctgtgtacatgtgtgtacatatattagaaagggaag-atgttaaagatatgtggcctgtg	2308
Sbjct:	2188	tgtctctgtacatgttatgtacatatcagaaggggaaggatgttaaгааатgtggcctgtg	2247
Query:	2309	ggttacacaggggtgcctgcagcpgttaatatatttttagaaатааतатсaaатаactcaa	2368
Sbjct:	2248	ggttacacaggggtgcctgcagcpgttaatatatttttagaaатаататсaaатаactcca	2307

```
Query: 2811 aggc aaagcagt gctctg agtatcac atcacacaa aaggaca aaagcgaa acacacaaa 2870
          |||||
Sbjct: 2768 aggc aaagcagt gctctga atatcata ccacacaca aggaca aaatgcga acccacaga 2827
```

 **NCBI**
Nucleotide Protein Translations Retrieve results for an RID

formatting **BLAST**

Your request has been successfully submitted and put into the Blast Queue.

Query = (1946 letters)

The request ID is

Format! or **Reset all**

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ Linkout ☐ Sequence Retrieval ☒ NCBI-gi in

Number of: Descriptions Alignments

Alignment view

Limit results by or select from:

Expect value

range:

 **NCBI**
Nucleotide Protein Translations Retrieve results for an RID

formatting **BLAST**

Your request has been successfully submitted and put into the Blast Queue.

Query = (1946 letters)

megablast seq 7

The request ID is

or

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi in

Number of: Descriptions Alignments

Alignment view

Start formatting
from query #

Limit results by or select from:

Expect value
range:

Results file ☐



results of BLAST

BLASTN 2.2.6 [Apr-09-2003]

SEQ 8

RID: 1061911967-29701-25492.BLASTQ3

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)
1,886,208 sequences; 8,918,056,233 total letters

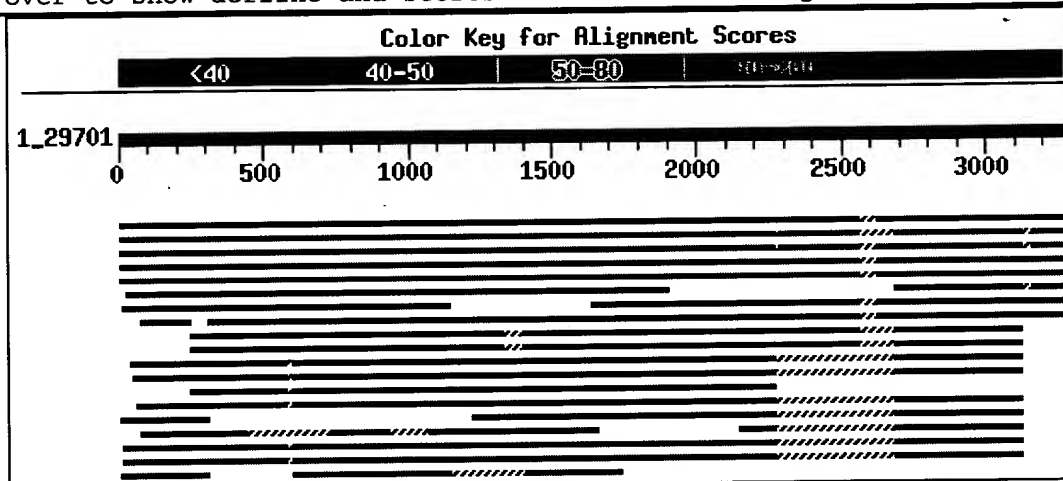
Taxonomy reports

Query=

(3283 letters)

Distribution of 82 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score E
(bits) Value

→	gi	4883680	gb	AF057352.1	AF057352	Homo sapiens hepatocellul...	4857	0.0
	gi	7656675	gb	AC020629.6		Homo sapiens 12q BAC RP11-76E16 (...	3592	0.0
	gi	15552942	emb	AL596177.4		Human DNA sequence from clone R...	3505	0.0
→	gi	27552765	ref	NM_006548.2		Homo sapiens IGF-II mRNA-bindi...	2675	0.0
	gi	33878041	gb	BC021290.2		Homo sapiens IGF-II mRNA-binding...	2675	0.0
→	gi	4191609	gb	AF117107.1	AF117107	Homo sapiens IGF-II mRNA...	2109	0.0
	gi	27485839	ref	XM_208686.1		Homo sapiens similar to hepato...	1865	0.0
	gi	27413166	gb	AC016961.28		Homo sapiens 3 BAC RP11-394J21 ...	1708	0.0
	gi	31873661	emb	BX537583.1	HSM806243	Homo sapiens mRNA; cDN...	1708	0.0
	gi	19849375	gb	AC104980.5		Homo sapiens chromosome 8, clone...	1665	0.0
	gi	17298202	dbj	AP004290.2		Homo sapiens genomic DNA, chrom...	1659	0.0
	gi	26093366	dbj	AK049196.1		Mus musculus ES cells cDNA, RIK...	1267	0.0
	gi	23958572	gb	BC023758.1		Mus musculus RIKEN cDNA C330012H...	1261	0.0
	gi	26090647	dbj	AK044984.1		Mus musculus 9.5 days embryo pa...	1256	0.0
	gi	26097330	dbj	AK077404.1		Mus musculus 6 days neonate hea...	1248	0.0
	gi	28492961	ref	XM_193835.2		Mus musculus RIKEN cDNA C33001...	1175	0.0
	gi	30148117	ref	XM_291469.2		Homo sapiens similar to hepato...	962	0.0

gi	33942111	ref	NM 183029.1	Mus musculus RIKEN cDNA C33001...	954	0.0
gi	32451876	gb	BC054552.1	Mus musculus cDNA clone MGC:6242...	954	0.0
gi	27666189	ref	XM 221343.1	Rattus norvegicus similar to I...	740	0.0
gi	18464262	gb	AC105413.3	Homo sapiens BAC clone RP11-64A1...	669	0.0
gi	23355671	gb	AC108670.10	Homo sapiens 3 BAC RP11-218A22 ...	479	e-131
gi	17737024	gb	AC009247.13	AC009247 Homo sapiens 3q27 BAC ...	479	e-131
gi	26082515	dbj	AK031773.1	Mus musculus 11 days embryo hea...	406	e-109
gi	27665993	ref	XM 221344.1	Rattus norvegicus similar to I...	302	2e-78

Alignments

>gi|4883680|gb|AF057352.1|AF057352 Homo sapiens hepatocellular carcinoma autoantigen
complete cds
Length = 3667

Score = 4857 bits (2526), Expect = 0.0
Identities = 2541/2556 (99%)
Strand = Plus / Plus

```

Query: 6      cggaggaggcaggagcgccgggtaccgggccccggggagccgaggctctcggggaagag 65
             |||
Sbjct: 372    cggaggaggcaggagcgccgggtaccgggccccggggagccgaggctctcggggaagag 431

Query: 66     acggatgatgaacaagctttacatcggaacctgagccccgccgtcaccgccgacgacct 125
             |||
Sbjct: 432    acggatgatgaacaagctttacatcggaacctgagccccgccgtcaccgccgacgacct 491

Query: 126     ccggcagctctttggggacaggaagctgccctggcgggacaggtcctgctgaagtccgg 185
             |||
Sbjct: 492     ccggcagctctttggggacaggaagctgccctggcgggacaggtcctgctgaagtccgg 551

Query: 186     ctacgccttcgtggactacccgaccagaactgggccatccgcgccatcgagaccctctc 245
             |||
Sbjct: 552     ctacgccttcgtggactacccgaccagaactgggccatccgcgccatcgagaccctctc 611

Query: 246     gggtaaaagtgaattgcatgggaaaatcatggaagttgattactcagtctctaaaaagct 305
             |||
Sbjct: 612     gggtaaaagtgaattgcatgggaaaatcatggaagttgattactcagtctctaaaaagct 671

Query: 306     aaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtgagggtgttggg 365
             |||
Sbjct: 672     aaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtgagggtgttggg 731

Query: 366     tggacttttggctcaatatgggacagtgaggagaatgtggaacaagtcaacacagacacaga 425
             |||
Sbjct: 732     tggacttttggctcaatatgggacagtgaggagaatgtggaacaagtcaacacagacacaga 791

Query: 426     aaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaatagccatggagaa 485
             |||
Sbjct: 792     aaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaatagccatggagaa 851

Query: 486     gctaagcgggcatcagtttgagaactactccttcaagatttcctacatcccggatgaaga 545
             |||
Sbjct: 852     gctaagcgggcatcagtttgagaactactccttcaagatttcctacatcccggatgaaga 911

```

Query: 546 ggtgagctcccccttcgccccctcagcgagcccagcgtggggaccactcttcccgggagca 605
|||
Sbjct: 912 ggtgagctcccccttcgccccctcagcgagcccagcgtggggaccactcttcccgggagca 971

Query: 606 aggccacgcccctgggggcacttctcaggccagacagattgatttcccgtgcggatcct 665
|||
Sbjct: 972 aggccacgcccctgggggcacttctcaggccagacagattgatttcccgtgcggatcct 1031

Query: 666 ggtccccaccagtttgttggtgccatcatcggaaggagggttgaccataaagaacat 725
|||
Sbjct: 1032 ggtccccaccagtttgttggtgccatcatcggaaggagggttgaccataaagaacat 1091

Query: 726 cactaagcagaccagtcgggtagatatccatagaaaagagaactctggagctgcaga 785
|||
Sbjct: 1092 cactaagcagaccagtcgggtagatatccatagaaaagagaactctggagctgcaga 1151

Query: 786 gaagcctgtcaccatccatgccaccccagaggggacttctgaagcatgccgcatttct 845
|||
Sbjct: 1152 gaagcctgtcaccatccatgccaccccagaggggacttctgaagcatgccgcatttct 1211

Query: 846 tgaaatcatgcagaaagaggcagatgagaccaaactagccgaagagattcctctgaaaat 905
|||
Sbjct: 1212 tgaaatcatgcagaaagaggcagatgagaccaaactagccgaagagattcctctgaaaat 1271

Query: 906 cttggcacacaatggcttggttgaagactgattggaaaagaaggcagaaatttgaagaa 965
|||
Sbjct: 1272 cttggcacacaatggcttggttgaagactgattggaaaagaaggcagaaatttgaagaa 1331

Query: 966 aattgaacatgaaacagggaccaagataacaatctcatctttgcaggatttgagcatata 1025
|||
Sbjct: 1332 aattgaacatgaaacagggaccaagataacaatctcatctttgcaggatttgagcatata 1391

Query: 1026 caaccggaaagaaccatcactgtgaagggcacagttgaggcctgtgccagtgtgagat 1085
|||
Sbjct: 1392 caaccggaaagaaccatcactgtgaagggcacagttgaggcctgtgccagtgtgagat 1451

Query: 1086 agagattatgaagaagctgcgtgaggcctttgaaaatgatatgctggctgttaacaccca 1145
|||
Sbjct: 1452 agagattatgaagaagctgcgtgaggcctttgaaaatgatatgctggctgttaacaccca 1511

Query: 1146 ctccggatacttctccagcctgtacccccatcaccagtttggcccgttcccgcattcatca 1205
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Sbjct: 1512 ctccggatacttctccagcctgtacccccatcaccagtttggcccgttcccgcattcatca 1571

Query: 1206 ctcttatccagagcaggagattgtgaatctcttcatcccaaccaggctgtgggcgcat 1265
|||
Sbjct: 1572 ctcttatccagagcaggagattgtgaatctcttcatcccaaccaggctgtgggcgcat 1631

Query: 1266 catcggaagaagggggcacacatcaaacagctggcgagattcgccggagcctctatcaa 1325
|||
Sbjct: 1632 catcggaagaagggggcacacatcaaacagctggcgagattcgccggagcctctatcaa 1691

Query: 1326 gattgccctgcggaaggcccagacgtcagcgaaaggatggatcatcatcaccggggccacc 1385
|||||
Sbjct: 1692 gattgccctgcggaaggcccagacgtcagcgaaaggatggatcatcatcaccggggccacc 1751

Query: 1386 ggaagcccagttcaaggcccaggacggatctttgggaaactgaaagaggaaaacttctt 1445
|||||
Sbjct: 1752 ggaagcccagttcaaggcccaggacggatctttgggaaactgaaagaggaaaacttctt 1811

Query: 1446 taaccccaaagaagaagtgaagctggaagcgcatatcagagtgcctcttccacagctgg 1505
|||||
Sbjct: 1812 taaccccaaagaagaagtgaagctggaagcgcatatcagagtgcctcttccacagctgg 1871

Query: 1506 ccgggtgattggcaaaggtggcaagaccgtgaacgaactgcagaacttaaccagtgcaga 1565
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Sbjct: 1872 ccgggtgattggcaaaggtggcaagaccgtgaacgaactgcagaacttaaccagtgcaga 1931

Query: 1566 agtcatcgtgcctcgtgaccaaaccgagatgaaaatgaggaagtgatcgtcagaattat 1625
|||||
Sbjct: 1932 agtcatcgtgcctcgtgaccaaaccgagatgaaaatgaggaagtgatcgtcagaattat 1991

Query: 1626 cgggcacttctttgctagccagactgcacagcgcaagatcagggaaattgtacaacaggt 1685
|||||
Sbjct: 1992 cgggcacttctttgctagccagactgcacagcgcaagatcagggaaattgtacaacaggt 2051

Query: 1686 gaagcagcaggagcagaaataccctcagggagtcgcctcacagcgagcaagtgaggctc 1745
|||||
Sbjct: 2052 gaagcagcaggagcagaaataccctcagggagtcgcctcacagcgagcaagtgaggctc 2111

Query: 1746 ccacaggcaccagcaaaacaacggatgaatgtagcccttccaacacctgacagaatgaga 1805
|||||
Sbjct: 2112 ccacaggcaccagcaaaacaacggatgaatgtagcccttccaacacctgacagaatgaga 2171

Query: 1806 ccaaaccgcagccagccagatcgggagcaaaacaaagaccatctgaggaatgagaagtctg 1865
|||||
Sbjct: 2172 ccaaaccgcagccagccagatcgggagcaaaacaaagaccatctgaggaatgagaagtctg 2231

Query: 1866 cggaggcggccagggaactctgccgaggccctgagaaccccgaggccgaggagggcggg 1925
|||||
Sbjct: 2232 cggaggcggccagggaactctgccgaggccctgagaaccccgaggccgaggagggcggg 2291

Query: 1926 gaaggtcagccaggtttgccagaaccaccgagccccgcctcccgccccccagggttctg 1985
|||||
Sbjct: 2292 gaaggtcagccaggtttgccagaaccaccgagccccgcctcccgccccccagggttctg 2351

Query: 1986 caggcttcagccatccacttcaccatccactcggatctctcctgaactcccacgacgcta 2045
|||||
Sbjct: 2352 caggcttcagccatccacttcaccatccactcggatctctcctgaactcccacgacgcta 2411

Query: 2046 tcccttttagttgaactaacataggtgaacgtgttcaaagccaagcaaaatgcacaccct 2105
|||||
Sbjct: 2412 tcccttttagttgaactaacataggtgaacgtgttcaaagccaagcaaaatgcacaccct 2471

Query: 2106 ttttctgtggcaaatacgtctctgtacatgtgtgtacatattagaaaggaagatgttaag 2165
|||||
Sbjct: 2472 ttttctgtggcaaatacgtctctgtacatgtgtgtacatattagaaaggaagatgttaag 2531

Query: 2166 atatgtggcctgtgggttacacagggtgcctgcagcggtaatatattttagaaataatat 2225
|||||
Sbjct: 2532 atatgtggcctgtgggttacacagggtgcctgcagcggtaatatattttagaaataatat 2591

Query: 2226 atcaaataactcaactaactccaatttttaataattattaannnnnnnnnnnnnnnaaa 2285
|||||
Sbjct: 2592 atcaaataactcaactaactccaatttttaataattattaatttttttttctttttaaa 2651

Query: 2286 gagaaagcaggccttttctagactttaagaataaagtctttgggaggtctcacggtgtag 2345
|||||
Sbjct: 2652 gagaaagcaggccttttctagactttaagaataaagtctttgggaggtctcacggtgtag 2711

Query: 2346 agaggagctttgaggccaccgcacaaaattcacccagagggaaatctcgctcgaaggac 2405
|||||
Sbjct: 2712 agaggagctttgaggccaccgcacaaaattcacccagagggaaatctcgctcgaaggac 2771

Query: 2406 actcacggcagttctggatcacctgtgtatgtcaacagaagggataccgtctccttgaag 2465
|||||
Sbjct: 2772 actcacggcagttctggatcacctgtgtatgtcaacagaagggataccgtctccttgaag 2831

Query: 2466 aggaaactctgtcactcctcatgcctgtctagctcatacacccatttctctttgcttcac 2525
|||||
Sbjct: 2832 aggaaactctgtcactcctcatgcctgtctagctcatacacccatttctctttgcttcac 2891

Query: 2526 aggttttaactgggtttttgcatactgctatataa 2561
|||||
Sbjct: 2892 aggttttaactgggtttttgcatactgctatataa 2927

Score = 1052 bits (547), Expect = 0.0
Identities = 608/665 (91%), Gaps = 2/665 (0%)
Strand = Plus / Plus

Query: 2620 cattcttttgaatttctcatccctccatctcaatcccgtatctacgcannnnnnnnnnnn 2679
|||||
Sbjct: 2986 cattcttttgaatttctcatccctccatctcaatcccgtatctacgcacccccccccc 3045

Query: 2680 nnaggcaaagcagtgctctgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 2739
|||||
Sbjct: 3046 c-aggcaaagcagtgctctgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 3104

Query: 2740 aaccagcctcaacttacacttggttactcaaaagaacaagagtcaatgggtacttgtccta 2799
|||||
Sbjct: 3105 aaccagcctcaacttacacttggttactcaaaagaacaagagtcaatgggtacttgtccta 3164

Query: 2800 gcgttttggaagaggaaaacaggaacccaccaaaccaaatcaaccaacaaagaaaa 2859
|||||
Sbjct: 3165 gcgttttggaagaggaaaacaggaacccaccaaaccaaatcaaccaacaaagaaaa 3224

Query: 2860 aattccacaatgaaagaatgtattttgtctttttgcattttggtgtataagccatcaata 2919
|||||
Sbjct: 3225 aattccacaatgaaagaatgtattttgtctttttgcattttggtgtataagccatcaata 3284

Query: 2920 ttcagcaaaatgattcctttctttnnnnnnnnnn-tgtggaggaaagtagaaatttacc 2978
|||||
Sbjct: 3285 ttcagcaaaatgattcctttctttaaaaaaaaaaagtgtggaggaaagtagaaatttacc 3344

Query: 2979 aaggttggtggcccgaggcggttaaattcacagannnnnnnaacgagaaaaacacacagaa 3038
|||||
Sbjct: 3345 aaggttggtggcccgaggcggttaaattcacagatttttttaacgagaaaaacacacagaa 3404

Query: 3039 gaagctacctcaggtgtttttacctcagcaccttgctcttggtttcccttagagatttt 3098
|||||
Sbjct: 3405 gaagctacctcaggtgtttttacctcagcaccttgatcttggtttcccttagagatttt 3464

Query: 3099 gtaaagctgatagttggagcannnnnnnnnnnnnaataaaaaatgagttggnnnnnnnn 3158
|||||
Sbjct: 3465 gtaaagctgatagttggagcatttttttatttttttaataaaaaatgagttggaaaaaaa 3524

Query: 3159 taagatatcaactgccagcctggagaaggtgacagtcgaagtgtgcaacagctgttctga 3218
|||||
Sbjct: 3525 taagatatcaactgccagcctggagaaggtgacagtcgaagtgtgcaacagctgttctga 3584

Query: 3219 attgtcttccgctagccaagaacnatatggccttcttttgacaaaccttgaaaatggt 3278
|||||
Sbjct: 3585 attgtcttccgctagccaagaacctatatggccttcttttgacaaaccttgaaaatggt 3644

Query: 3279 tattt 3283
|||||
Sbjct: 3645 tattt 3649

>gi|7656675|gb|AC020629.6| Homo sapiens 12q BAC RP11-76E16 (Roswell Park Cancer Inst
Library) complete sequence
Length = 142971

Score = 3592 bits (1868), Expect = 0.0
Identities = 2140/2268 (94%), Gaps = 31/2268 (1%)
Strand = Plus / Plus

Query: 1 ggcagcggaggaggcgaggagcgccgggtaccggggcgggggagccgaggctctcgggg 60
|||||
Sbjct: 132954 ggcagcagaggaggcgaggagcgagggtatcggg-cgggggagccgaggccctcgggg 133012

Query: 61 aagagacggatgatgaacaagctttacatcggaacctgagccccgccgtcaccgccgac 120
||
Sbjct: 133013 aacagacggatgatgaacaagctttacatcggaacctgagccccgccgtcaccgccgaa 133072

Query: 121 gacctccggcagctctttggggacaggaagctgccctggcgggacaggtcctgctgaag 180
|||||
Sbjct: 133073 gacctccggcagctctttggggacaggaagctgccctggcgggacaggtcctgctcaag 133132

Query: 181 tccggctacgccttcgtggactaccccgaccagaactgggcatccgcgccatcgagacc 240
|||

Sbjct: 133133 tcccgtacgccttcgtggactaccccgaccagaactgggccatccgcaccatcgagacc 133192

Query: 241 ctctcgggttaaagtggaattgcatgggaaaatcatggaagttgattactcagtctctctaaa 300
|||||
Sbjct: 133193 ctctcgggtcaagtggaattgcatgggaaaatcatggaagttgattattcagtctctata 133252

Query: 301 aagctaaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtgggaggtg 360
|||||
Sbjct: 133253 aagctaaggagcaggaaacattccgattcgaaatatccctcctcacctgcagtgggaggtg 133312

Query: 361 ttggatggacttttggctcaatatgggacagtggagaatgtggaacaagtcaacacagac 420
|||||
Sbjct: 133313 ttggatggacttttggctcaatatgggacagtggagaatgtggaacaagtcaacacagac 133372

Query: 421 acagaaaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaatagccatg 480
|||||
Sbjct: 133373 acagagaccgctgttgtcaacgtcacatatgcaacaaaagaagaagtaaaaatagccatg 133432

Query: 481 gagaagctaagcgggcatcagtttgagaactactccttcaagatttcctacatcccggat 540
|||||
Sbjct: 133433 aagaagctaagcgggcatcagtttgagaaccactacttcaagatttcctacatcccggat 133492

Query: 541 gaagaggtgagctccccttcgccccctcagcgagcccagcgtggggaccactcttcccgg 600
|| |||||
Sbjct: 133493 gacgaggtgagctgcccttcgccccctcagcgagcccagcgtggggaccactcttccctgg 133552

Query: 601 gagcaaggccacgcccctgggggcacttctcaggccagacagattgatttcccgtgcg- 659
|||||
Sbjct: 133553 gagcaaggccaagcccctgggggctcttctcaggccagacagattgatttcccactgcgt 133612

Query: 660 gatcctgggtccccaccagtttgttggtgccatcatcggaaggagggttgaccataaa 719
| |||||
Sbjct: 133613 g-tcctgttccccaccagtttgttggtgccatcatcggaaggagggttgaccataaa 133671

Query: 720 gaacatcactaagcagaccagtcgccgggtagatatccatagaaaagagaactctggagc 779
|||||
Sbjct: 133672 gaacatcactaagcagagccggtcccggttagacatctatagacaagagaactccagagc 133731

Query: 780 tgcagagaagcctgtcaccatccatgccaccccagaggggacttctgaagcatgccgcat 839
|||||
Sbjct: 133732 tgcagagaagcctgt---ca-ccatgccaccccagaggggacttctgaagcatgccgcat 133787

Query: 840 gattcttgaaatcatgcagaaagaggcagatgagaccaaactagccgaagagattcctct 899
|||||
Sbjct: 133788 gattcttgaaataatgcagaaagaggcagatgaggccaaactagccgaagagattcctct 133847

Query: 900 gaaaatcttggcacacaatggcttggttgggaagactgattggaaaagaaggcagaaattt 959
|||||
Sbjct: 133848 gaaaatcttggcccacaatggcttggttgggaagactgattggaaaagaaggcagaaattt 133907

Query: 960 gaagaaaattgaacatgaaacagggaccaagataacaatctcatctttgcaggatttgag 1019
|||||

Sbjct: 133908 gaagaaaaatgaacatgaaacagggaccaagataacaatctcatcttcgcaggatttgag 133967

Query: 1020 catatacaacccggaagaaccatcactgtgaagggcacagttgaggcctgtgccagtgc 1079
|||||

Sbjct: 133968 catatacaacccggaagaaccatcactgtgaagggcacagtcgaggtctgtgccagtgc 134027

Query: 1080 tgagatagagattatgaagaagctgcgtgaggcctttgaaaatgatatgctggctgttaa 1139
|||||

Sbjct: 134028 tgagatagagattatgaagaagctgcgtgaggcctttgaaaatgatacgctgactgttaa 134087

Query: 1140 caccactccggatacttctccagcctgtacccccatcaccagtttgcccgttcccga 1199
|||||

Sbjct: 134088 taccacttcggatacttctccagcctgtacccccatcgccagtttgcccgttcccga 134147

Query: 1200 tcatcactcttatccagagcaggagattgtgaatctcttcacccaaccaggctgtggg 1259
|||||

Sbjct: 134148 tcatcactcttatccagagcaggagattgtcaatctcttcacccaaccagggtgtggg 134207

Query: 1260 cgccatcatcggaagaagggggcacacatcaaacagctggcgagattcgccggagcctc 1319
|||||

Sbjct: 134208 cgccatcatcggaagaagggggcacacatcaaacagctggcgagattcgtgggagcctc 134267

Query: 1320 tatcaagattgcccctgcggaaggcccagacgtcagcgaaaggatggatcatcatcacgg 1379
|||||

Sbjct: 134268 catcaaga-t----c-gc-----ccctg-cgtcagc---ggaaggatcatcatcacctg 134310

Query: 1380 gccaccggaagcccagttcaaggcccaggacggatctttgggaaactgaaagaggaaaa 1439
|||||

Sbjct: 134311 gccaccggaatcccagttcaaggcccaggacggatctttgggaaactgaaagaagaaaa 134370

Query: 1440 cttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgcctcttccac 1499
|||||

Sbjct: 134371 cttttttaaccccaaagaagacgtgaagctggaaacccatatcagagtgcctcttccac 134430

Query: 1500 agctggccgggtgattggcaaagggtggcaagaccgtgaacgaactgcagaacttaaccag 1559
|||||

Sbjct: 134431 cgctggccgggtgattggcaaagggggcaagaccgtgaatgaactgcagaatttaaccag 134490

Query: 1560 tgcagaagtcacgtgcctcgtgaccaaaccgagatgaaaatgaggaagtgcgtcag 1619
|||||

Sbjct: 134491 tgcagaagtcacgtgcctcgtgaccaaaccgagatgaaaatgaggaaatgcgtcag 134550

Query: 1620 aattatcgggcacttctttgctagccagactgcacagcgcaagatcagggaaattgtaca 1679
|||||

Sbjct: 134551 aattatcgggcacttctttgctagccagactgcacagcgcaagatcagggaaattgtaca 134610

Query: 1680 acagggtgaagcagcaggagcagaaataccctcagggagtcgcctcacagcgagcaagtg 1739
|||||

Sbjct: 134611 acagggtgaagcagcaggagcagaaataccctcagggagtcgcctcacagcgagcaagtg 134670

Query: 1740 aggctcccacaggcaccagcaaaacaacggatgaatgtagcccttccaacacctgacaga 1799
|||||

Sbjct: 134671 aggatccacaggcacaagcaaaacaacggaagaatgtagcccttccaacacctgacaga 134730

Query: 1800 atgagaccaaacgcagccagccagatcgggagcaaaccaaagaccatctgaggaatgaga 1859
|||||

Sbjct: 134731 atgagaccaaacacagccagccagatcaagagcaaaccaaagaccatctgaggaatgaga 134790

Query: 1860 agtctgcgaggcgccagggactctgccgaggccctgagaacccaggggcccaggagg 1919
|||||

Sbjct: 134791 agtctgcgaggcgccagggactctgtagaggccctgagaacccaggggcccaggagg 134850

Query: 1920 ggcggggaaggtcagccaggtttgccagaaccaccgagccccgcctcccgcacccaggg 1979
|||

Sbjct: 134851 ggtggggaaggtaaaccaggtttgccagaaccaccgggccccctcctcctgtcccccaggg 134910

Query: 1980 cttctgcaggcttcagccatccacttcaccatccactcggatctctcctgaactcccacg 2039
|||||

Sbjct: 134911 cttctgcaggcttcagccatccacttcaccatccactcggatctctccttaactcccacg 134970

Query: 2040 acgctatcccttttagttgaactaacataggtgaacgt-gttcaaagccaagcaaaatgc 2098
|||||

Sbjct: 134971 acgctatcccttttagttgaactaaaataggtgaacattgttcaaagccaagcaaaatgc 135030

Query: 2099 acacccttttctgtggcaaatcgtctctgtacatgtgtgtacatattagaaaggggaaga 2158
|||

Sbjct: 135031 acgccctttt-tgtggcaaatagtctctctacacgtgtatacatattagaaggggaaga 135089

Query: 2159 tgттаagatatgtggcctgtgggttacacaggggtgcctgcagcggtaatatatttttagaa 2218
|||||

Sbjct: 135090 tgттаagatatgtggcctgtgggttacacaggggtgcctgcagcggtaatatatttttagaa 135149

Query: 2219 ataatatatcaaataactcaactaactccaatttttaataattatta 2266
|||||

Sbjct: 135150 ataatatatcaaataact-aact--c-c-aatttttaataattatta 135192

Score = 675 bits (351), Expect = 0.0
Identities = 407/442 (92%), Gaps = 6/442 (1%)
Strand = Plus / Plus

Query: 2682 aggcaaagcagtgtctctgagtatcacatcacacaaaaggaacaaaagcgaaacacacaaa 2741
|||||

Sbjct: 135606 aggcaaagcagtgtctctgagtatcacatcacacaaaaggaacaaaagcgaaacacacaaa 135665

Query: 2742 ccagcctcaacttacacttggttactcaaaagaacaagagtcaatgggtacttgtcctagc 2801
|||||

Sbjct: 135666 ccagcctcaacttacacttggttactcaaaagaacaagagtcaatgggtacttgtcctagc 135725

Query: 2802 gttttggaagaggaaaacaggaacccaccaaaccaaccaatcaaccaaacaagaaaaaa 2861
|||||

Sbjct: 135726 attttggaagaggaaaacaggaacctatcaaaccaaccaatcaaccaaacaagaaaaaa 135785

Query: 2862 ttccacaatgaaagaatgtattttgtctttttgcattttgggtgtataagccatcaatatt 2921
|||||

Query: 3219 attgtcttccgctagccaagaaccnatatggccttcttttggacaaaccttgaaaaatgtt 3278

Sbjct: 136145 attgtcttctgctagccaagaacctatatgaccttcttttggacaaactttgaaaaatgtt 136204

Query: 3279 ta 3280

||

Sbjct: 136205 ta 136206

>gi|15552942|emb|AL596177.4| Human DNA sequence from clone RP11-325P15 on chromosome
sequence

Length = 91084

Score = 3505 bits (1823), Expect = 0.0

Identities = 2138/2284 (93%), Gaps = 45/2284 (1%)

Strand = Plus / Plus

Query: 1 ggcagcggaggagggcaggagcgccgggtaccggggccgggggagccgcgggctctcgggg 60
|||||
Sbjct: 9381 ggcagcggaggagggcaggagcgccgggtaccaggccgggggaggcgcgggctcccgggg 9440

Query: 61 aagagacggatgatgaacaagctttacatcgggaaacctgagccccgccgtcaccgccgac 120
|||||
Sbjct: 9441 aagagacgggtgatgaacaatctttacatcgggaaaccttagccctgcgggtcaccgccgac 9500

Query: 121 gacctccggcagctctttggggacaggaagctgccccctggcgggacaggtcctgctgaag 180
|||||
Sbjct: 9501 gacctctggcagctctttggggacaggaagctgccccccaccggacaggtcctgctcaag 9560

Query: 181 tccggctacgccttcgtggactaccccgaccagaactggggccatccgcgccatcgagacc 240
|||||
Sbjct: 9561 tccggctatgccttcgtggactacccctacaagaactggggccatccgcgccatcgagacc 9620

Query: 241 ctctcgggtaaagtggaattgcatgggaaaatcatggaagttgattactcagtctctaaa 300
|||||
Sbjct: 9621 ctctcgggtaaagtggaattgcatgggaaaatcatggaagttgattactcagtctctaaa 9680

Query: 301 aagctaaggagcaggaaaaattcagattcgaaacatccctcctcacctgcagtgggaggtg 360
|||||
Sbjct: 9681 aagctaaggaggagaaaaattcagattcgaaacatccctcctcacctccagtgggaggtg 9740

Query: 361 ttggatggacttttggctcaatatgggacagtggagaatgtgg---aacaagtcaacaca 417
|||||
Sbjct: 9741 ttggatggacttttggctcaatatggaacagtggagaatgtggaacaacaagtcaacaca 9800

Query: 418 gacacagaaaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaaatagcc 477
|||||
Sbjct: 9801 gacacagaaaccactgttgtcaacgtcacatatgcaac-a-ag-agaag-aaaatagac 9855

Query: 478 atggagaagctaagcgggcatcagtttgagaactactccttcaagatttcctacatccc 537
|||||
Sbjct: 9856 atggagaggctaagcgggcatcagtttgagaactagtcccttcaagatttcctacatccc 9915

Query: 538 gatgaagaggtgagctccccttcgccccctcagcgagcccagcgtggggaccactcttcc 597
|||||
Sbjct: 9916 gatgaagaggtgagctccccttcgccccctcagcgagcccagcgtggggaccactcttcc 9975

Query: 598	c-gggagcaaggccacgcccctgggggcacttctcaggccagacagattgatttcccgcct	656
Sbjct: 9976	cggggagcaaggccacgaccctgggggcgcttcttaggccagacagattgatttccctgct	10035
Query: 657	gc-ggatccttggtcccc-ac-----ccagtttggtggtgccatcatcgaaaggagggct	709
Sbjct: 10036	gcagg-tcctggtcccctacagtttgagtttggtggtgccatcatcagaaaggagggct	10094
Query: 710	tgaccataaagaacatcactaagcagacccagtcgccgggtagatatccatagaaaagaga	769
Sbjct: 10095	tgaccataaagaacatcactaagtagaccagtcgccggatagatatccatagaaaagaga	10154
Query: 770	actctggagctgcagagaagcctgtcaccatccatgccaccccagaggggacttctgaag	829
Sbjct: 10155	actctggagctgcagagaagcctgtcaccatccatgccaccccaggggggacttctgaag	10214
Query: 830	catgccgcatgattcttgaaatcatgcagaaaggagcagatgagacaaactagccgaag	889
Sbjct: 10215	catgcctcatgattcttgaaatcatgcagaaaggagcagatgagaacaaactagccgaag	10274
Query: 890	agattcctctgaaaatcttggcacacaatggccttggttggaagactgattggaaaagaag	949
Sbjct: 10275	agattcctctgaaaatcttggcccacaatggc-----tt----g---g--ttggaaaagaag	10322
Query: 950	gcagaaatttgaagaaaattgaacatgaaacagggaccaagataacaatctcatctttgc	1009
Sbjct: 10323	gcagaaatttgaagaaaattgaacatgaaacagggaccaagatagcaatctcatctttgc	10382
Query: 1010	aggatttgagcatatacaacccggaaagaaccatcactgtgaagggcacag-ttgaggcc	1068
Sbjct: 10383	aggatttgagcataaataaccaggaaagaatcatcactgtgaagggcacagtttgaggcc	10442
Query: 1069	tgtgccagtgtgagatagagattatgaagaagctgcgtgaggcctttgaaaatgatatg	1128
Sbjct: 10443	tgtgccagtgtgagatagagattatgaagaagctgcgtgagacctttgaaaatgatatg	10502
Query: 1129	ctggctgttaacacccactccgatacttctccagcctgtacccccatcaccagtttggc	1188
Sbjct: 10503	ttggctgttaataacgcactccgatacttctccagcctgtacccccatcaccaggttggc	10562
Query: 1189	ccgttcccgcacatcatcactcttatccagagcaggagattgtgaatctcttcatcccaacc	1248
Sbjct: 10563	ccgttcccgcacatcatcactcttatccagagcaggaggttgtgaatctcttcatcccaacc	10622
Query: 1249	caggctgtgggcgccatcatcggaagaagggg-gcacacatcaaacagctggcgagatt	1307
Sbjct: 10623	caggctgtgggcgccattatcaggaag-aggggagcacacatcaaacagctggcgagatt	10681
Query: 1308	cgccggagcctctatcaagattgccctgcggaaggcccagacgtcagcgaaaggatgggt	1367
Sbjct: 10682	cgccacagcctccatcaagatcgccctgcggaaggcccagacgtcaacgaaaggatgggt	10741

Query: 1368 catcatcacccgggccaccggaagcccagttcaaggcccaggacggatctttgggaaact 1427
|||||
Sbjct: 10742 catcatcacccgggccaccggaagcccagttcaaggcccaggacggatctttgggaaact 10801

Query: 1428 gaaagaggaaaacttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagt 1487
|||||
Sbjct: 10802 gaaagaagaaaacttctttaaccccaaagaagaagtgaagctggaagcccgtatcagagt 10861

Query: 1488 gccctcttcacagctggccgggtgattggcaaaggtggcaagaccgtgaacgaactgca 1547
|||||
Sbjct: 10862 gccctcttcacagctggccgggtgattggcaaaggtgtcaataccttgaatgaactgca 10921

Query: 1548 gaacttaaccagtgcagaagtcacgtgcctcgtgaccaaaccgagatgaaaatgagga 1607
|||||
Sbjct: 10922 gaacttaaccagtgcagaagtcacgtgcctcgtgaccaaaggcagatgaaaatgagga 10981

Query: 1608 agtgatcgtcagaattatcgggcacttctttgcta-gccagactgcacagcgcaagatca 1666
|||||
Sbjct: 10982 agtgatcgtcagaattattggacacttctttgctaccca-actgcatagcacaagatca 11040

Query: 1667 gggaaattgtacaacaggtgaagcagcaggagcagaaataccctcaggagtcgcctcac 1726
|||||
Sbjct: 11041 gggaaactgtacaacaggtgaagcagcaagagcagaaataccctcaggagtcgcctcac 11100

Query: 1727 agcgcagcaagtgaggctccacaggcaccagcaaaacaacggatgaatgtagcccttcc 1786
|||
Sbjct: 11101 agcacagcaagtgaggctccacaggcaccagcaaaacaacggatgaatggagcccttcc 11160

Query: 1787 aacacctgacagaatgagaccaaaccgagccagccagatcgaggagcaaaccaaagaccat 1846
|||||
Sbjct: 11161 aacacctgacagaatgagaccaaaccgagccagccagatcgaggagcaaaccaaagaccat 11220

Query: 1847 ctgaggaatgagaagtctgcgaggcgccagggactctgccgaggccctgagaaccca 1906
|||||
Sbjct: 11221 ctgaggaatgagaagtctgcgaggctgccagggactctgaagaggccctgagaattcca 11280

Query: 1907 ggggcccaggagggggcggggaaggtcagccaggtttgccagaaccaccgagccccgcctc 1966
|||||
Sbjct: 11281 ggggcccaggaggggtggggaaggtcagccaggtttgccagaaccactgggccc-gcttc 11339

Query: 1967 ccgcccc--cagggcttctgcaggcttcagccatccacttcaccatccactcggatctc 2024
|||
Sbjct: 11340 tcacccccatcagggcttctgcaggcttcagccatccacttcaccatccactccgatctc 11399

Query: 2025 tcctgaactcccacgacgctatcccttttagttgaactaacataggtgaacgtgttcaaa 2084
|||
Sbjct: 11400 tccttaactcccacgacgctatcccttttagttgaactaacatag-tgat-gcgttcaaa 11457

Query: 2085 gccaaagcaaaatgcacaccctttttctgtggcaaactcgtctctgtacatgtgtgtacata 2144
|||||
Sbjct: 11458 gccaaagcaaaatgcacaccctttttctgtgacaagtcacgtctgtacatgtgtatacata 11517

```
Query: 3097  ttgtaaagctgatagttggagca 3119
             |||
Sbjct: 12470  ttgtaaaactgatagttggagca 12492
```

Score = 437 bits (227), Expect = e-119
Identities = 266/284 (93%), Gaps = 5/284 (1%)
Strand = Plus / Plus

Query: 2283 aaagagaaagcaggccttttctagacttt-aaagaataaaag----tctttgggaggtctca 2337
|||
Sbjct: 11651 aaagagaaagcaggccttttctagacttttaaagaataaaagtctttctttgggaggtctca 11710

Query: 2338 cgggtgtagagaggagctttgaggccacccgcacaaaattcacccagagggaaatctcgtc 2397
|||
Sbjct: 11711 cagtatagacaggagctttgaggccacccacacaaaattcacccagagggaaatctcaaa 11770

Query: 2398 ggaaggacactcacggcagttctggatcacctgtgtatgtcaacagaaggataccgtct 2457
|||
Sbjct: 11771 ggaaggacaatcacagcagttctggatcacctgtgtatgtcaacagaaggataccatct 11830

Query: 2458 ccttgaagaggaaactctgtcactcctcatgcctgtctagctcatacacccatttctctt 2517
|||
Sbjct: 11831 ccttgaagaagaaactctgtcactcctcatgcctgtctagctcttacacccatttctctt 11890

Query: 2518 tgcttcacagggttttaaactgggtttttgcatactgctatataa 2561
|||
Sbjct: 11891 tgcttcacagggttttaaactggatttttgcatactgctatataa 11934

Score = 231 bits (120), Expect = 6e-57
Identities = 123/125 (98%)
Strand = Plus / Plus

Query: 3159 taagatatcaactgccagcctggagaagggtgacagtccaagtgtgcaacagctgttctga 3218
|||
Sbjct: 12533 taagatatcaactgccagcctggagaagggtgacagtccaagtgtgcaacagctgttctga 12592

Query: 3219 attgtcttccgctagccaagaacnataatggccttcttttggacaaaccttgaaaatgtt 3278
|||
Sbjct: 12593 attgtcttctgctagccaagaacctatataatggccttcttttggacaaaccttgaaaatgtt 12652

Query: 3279 tatttt 3283
|||
Sbjct: 12653 tatttt 12657

>gi|27552765|ref|NM_006548.2| Homo sapiens IGF-II mRNA-binding protein 2 (IMP-2), mR
Length = 3642

Score = 2675 bits (1391), Expect = 0.0
Identities = 1406/1421 (98%)
Strand = Plus / Plus

Query: 1141 acccactccggatacttctccagcctgtacccccatcacccagtttggcccgttcccgc 1200
|||
Sbjct: 1274 acccactccggatacttctccagcctgtacccccatcacccagtttggcccgttcccgc 1333

Query: 1201 catcactcttatccagagcaggagattgtgaatctcttcacccaaccaggctgtgggc 1260
|||

Sbjct: 1334 catcactcttatccagagcaggagattgtgaatctcttcatcccaacccaggctgtgggc 1393

Query: 1261 gccatcatcggaagaagggggcacacatcaaacagctggcgagattcgccggagcctct 1320
|||||

Sbjct: 1394 gccatcatcggaagaagggggcacacatcaaacagctggcgagattcgccggagcctct 1453

Query: 1321 atcaagattgccctgcggaaggccagacgtcagcgaaaggatggatcatcatcaccggg 1380
|||||

Sbjct: 1454 atcaagattgccctgcggaaggccagacgtcagcgaaaggatggatcatcatcaccggg 1513

Query: 1381 ccaccggaagcccagttcaaggcccaggacggatctttgggaaactgaaagaggaaaac 1440
|||||

Sbjct: 1514 ccaccggaagcccagttcaaggcccaggacggatctttgggaaactgaaagaggaaaac 1573

Query: 1441 ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgcctcttccaca 1500
|||||

Sbjct: 1574 ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgcctcttccaca 1633

Query: 1501 gctggcgggtgattggcaaaggtggcaagaccgtgaacgaactgcagaacttaaccagt 1560
|||||

Sbjct: 1634 gctggcgggtgattggcaaaggtggcaagaccgtgaacgaactgcagaacttaaccagt 1693

Query: 1561 gcagaagtcacgtgcctcgtgaccaaaccgagatgaaaatgaggaagtgatcgtcaga 1620
|||||

Sbjct: 1694 gcagaagtcacgtgcctcgtgaccaaaccgagatgaaaatgaggaagtgatcgtcaga 1753

Query: 1621 attatcgggcacttctttgctagccagactgcacagcgcaagatcagggaaattgtacaa 1680
|||||

Sbjct: 1754 attatcgggcacttctttgctagccagactgcacagcgcaagatcagggaaattgtacaa 1813

Query: 1681 caggtgaagcagcaggagcagaaataccctcaggagtcgcctcacagcgcagcaagtga 1740
|||||

Sbjct: 1814 caggtgaagcagcaggagcagaaataccctcaggagtcgcctcacagcgcagcaagtga 1873

Query: 1741 ggctccacaggcaccagcaaaacaacggatgaatgtagcccttccaacacctgacagaa 1800
|||||

Sbjct: 1874 ggctccacaggcaccagcaaaacaacggatgaatgtagcccttccaacacctgacagaa 1933

Query: 1801 tgagaccaaaccgagccagccagatcgggagcaaaccagaccatctgaggaatgagaa 1860
|||||

Sbjct: 1934 tgagaccaaaccgagccagccagatcgggagcaaaccagaccatctgaggaatgagaa 1993

Query: 1861 gtctgaggaggcgccaggactctgccgaggccctgagaaccccaggggcccaggaggg 1920
|||||

Sbjct: 1994 gtctgaggaggcgccaggactctgccgaggccctgagaaccccaggggcccaggaggg 2053

Query: 1921 gcggggaaggctcagccaggtttgccagaaccaccgagccccgcctcccgcacccagggc 1980
|||||

Sbjct: 2054 gcggggaaggctcagccaggtttgccagaaccaccgagccccgcctcccgcacccagggc 2113

Query: 1981 ttctgcaggcttcagccatccacttcaccatccactcggatctctcctgaactcccacga 2040
|||||

Sbjct: 2114 ttctgcaggcttcagccatccacttcaccatccactcggatctctctctgaactcccacga 2173

Query: 2041 cgctatcccttttagttgaactaacataggtgaacgtgttcaaagccaagcaaaatgcac 2100
|||||

Sbjct: 2174 cgctatcccttttagttgaactaacataggtgaacgtgttcaaagccaagcaaaatgcac 2233

Query: 2101 accctttttctgtggcaaatcgtctctgtacatgtgtgtacatattagaaaggggaagatg 2160
|||||

Sbjct: 2234 accctttttctgtggcaaatcgtctctgtacatgtgtgtacatattagaaaggggaagatg 2293

Query: 2161 ttaagatatgtggcctgtgggttacacaggggtgcctgcagcggtaatatatttttagaaat 2220
|||||

Sbjct: 2294 ttaagatatgtggcctgtgggttacacaggggtgcctgcagcggtaatatatttttagaaat 2353

Query: 2221 aatatatcaaataactcaactaactccaatttttaataattattaannnnnnnnnnnnnn 2280
|||||

Sbjct: 2354 aatatatcaaataactcaactaactccaatttttaataattattaatttttttttcttt 2413

Query: 2281 nnaagagaaagcaggcttttctagactttaagaataaagtctttgggaggtctcacgg 2340
|||||

Sbjct: 2414 ttaagagaaagcaggcttttctagactttaagaataaagtctttgggaggtctcacgg 2473

Query: 2341 tgtagagaggagctttgaggccacccgcacaaaattcacccagagggaatctcgtcgg 2400
|||||

Sbjct: 2474 tgtagagaggagctttgaggccacccgcacaaaattcacccagagggaatctcgtcgg 2533

Query: 2401 aggacactcacggcagttctggatcacctgtgtatgtcaacagaagggaataccgtctcct 2460
|||||

Sbjct: 2534 aggacactcacggcagttctggatcacctgtgtatgtcaacagaagggaataccgtctcct 2593

Query: 2461 tgaagaggaaactctgtcactcctcatgcctgtctagctcatacacccatttctctttgc 2520
|||||

Sbjct: 2594 tgaagaggaaactctgtcactcctcatgcctgtctagctcatacacccatttctctttgc 2653

Query: 2521 ttcacaggttttaactgggtttttgcatactgctatataa 2561
|||||

Sbjct: 2654 ttcacaggttttaactgggtttttgcatactgctatataa 2694

Score = 2184 bits (1136), Expect = 0.0
Identities = 1136/1136 (100%)
Strand = Plus / Plus

Query: 5 gcggaggaggcgaggagcgccgggtaccgggcccggggagccgcgggctctcggggaaga 64
|||||

Sbjct: 9 gcggaggaggcgaggagcgccgggtaccgggcccggggagccgcgggctctcggggaaga 68

Query: 65 gacggatgatgaacaagctttacatcggaacctgagccccgccgtcaccgccgacgacc 124
|||||

Sbjct: 69 gacggatgatgaacaagctttacatcggaacctgagccccgccgtcaccgccgacgacc 128

Query: 125 tccggcagctctttggggacaggaagctgccctggcgggacaggtcctgctgaagtccg 184
|||||

Sbjct: 129 tccggcagctctttggggacaggaagctgccctggcgggacaggtcctgctgaagtccg 188

Query: 185 gctacgccttcgtggactaccccgaccagaactgggcatccgcgccatcgagaccctct 244
|||||

Sbjct: 189 gctacgccttcgtggactaccccgaccagaactgggcatccgcgccatcgagaccctct 248

Query: 245 cgggtaaagtggaattgcatgggaaaatcatggaagttgattactcagtctctaaaaagc 304
|||||

Sbjct: 249 cgggtaaagtggaattgcatgggaaaatcatggaagttgattactcagtctctaaaaagc 308

Query: 305 taaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtgggaggtgttgg 364
|||||

Sbjct: 309 taaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtgggaggtgttgg 368

Query: 365 atggacttttggctcaatatgggacagtggagaatgtggaacaagtcaacacagacacag 424
|||||

Sbjct: 369 atggacttttggctcaatatgggacagtggagaatgtggaacaagtcaacacagacacag 428

Query: 425 aaaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaatagccatggaga 484
|||||

Sbjct: 429 aaaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaatagccatggaga 488

Query: 485 agctaagcgggcatcagtttgagaactactccttcaagatttcctacatcccggatgaag 544
|||||

Sbjct: 489 agctaagcgggcatcagtttgagaactactccttcaagatttcctacatcccggatgaag 548

Query: 545 aggtgagctccccttcgccccctcagcgagcccagcgtggggaccactcttcccgggagc 604
|||||

Sbjct: 549 aggtgagctccccttcgccccctcagcgagcccagcgtggggaccactcttcccgggagc 608

Query: 605 aagggcacgcccctgggggcacttctcaggccagacagattgatttcccgctgcggatcc 664
|||||

Sbjct: 609 aagggcacgcccctgggggcacttctcaggccagacagattgatttcccgctgcggatcc 668

Query: 665 tgggtccccacccagtttggttggtgccatcatcgaaaggagggttgaccataaagaaca 724
|||||

Sbjct: 669 tgggtccccacccagtttggttggtgccatcatcgaaaggagggttgaccataaagaaca 728

Query: 725 tcactaagcagaccagtcctcggttagatatccatagaaaagagaactctggagctgcag 784
|||||

Sbjct: 729 tcactaagcagaccagtcctcggttagatatccatagaaaagagaactctggagctgcag 788

Query: 785 agaagcctgtcaccatccatgccacccagaggggacttctgaagcatgccgcatgattc 844
|||||

Sbjct: 789 agaagcctgtcaccatccatgccacccagaggggacttctgaagcatgccgcatgattc 848

Query: 845 ttgaaatcatgcagaaagaggcagatgagaccaaactagccgaagagattcctctgaaaa 904
|||||

Sbjct: 849 ttgaaatcatgcagaaagaggcagatgagaccaaactagccgaagagattcctctgaaaa 908

Query: 905 tcttggcacacaatggcttgggttgggaagactgattggaaaagaaggcagaaatttgaaga 964
|||||

Sbjct: 909 tcttggcacacaatggcttgggttgaagactgattggaaaagaaggcagaaatttgaaga 968

Query: 965 aaattgaacatgaaacagggaccaagataacaatctcatctttgcaggatttgagcatat 1024
|||||

Sbjct: 969 aaattgaacatgaaacagggaccaagataacaatctcatctttgcaggatttgagcatat 1028

Query: 1025 acaaccggaagaaccatcactgtgaagggcacagttgaggcctgtgccagtgtgaga 1084
|||||

Sbjct: 1029 acaaccggaagaaccatcactgtgaagggcacagttgaggcctgtgccagtgtgaga 1088

Query: 1085 tagagattatgaagaagctgcgtgaggcctttgaaaatgatatgctggctgttaac 1140
|||||

Sbjct: 1089 tagagattatgaagaagctgcgtgaggcctttgaaaatgatatgctggctgttaac 1144

Score = 1058 bits (550), Expect = 0.0
Identities = 609/665 (91%), Gaps = 2/665 (0%)
Strand = Plus / Plus

Query: 2620 cattcttttgaatttcctcatccctccatctcaatcccgtatctacgcannnnnnnnnnn 2679
|||||

Sbjct: 2753 cattcttttgaatttcctcatccctccatctcaatcccgtatctacgca-ccccccccc 2811

Query: 2680 nnaggcaaagcagtgtctgtgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 2739
|||||

Sbjct: 2812 ccaggcaaagcagtgtctgtgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 2871

Query: 2740 aaccagcctcaacttacacttggttactcaaaagaacaagagtcaatgggtacttgtccta 2799
|||||

Sbjct: 2872 aaccagcctcaacttacacttggttactcaaaagaacaagagtcaatgggtacttgtccta 2931

Query: 2800 gcgttttgaagaggaaaacaggaacccaccaaaccaaatcaaccaaacaaagaaaa 2859
|||||

Sbjct: 2932 gcgttttgaagaggaaaacaggaacccaccaaaccaaatcaaccaaacaaagaaaa 2991

Query: 2860 aattccacaatgaaagaatgtattttgcattttgggtgtataagccatcaata 2919
|||||

Sbjct: 2992 aattccacaatgaaagaatgtattttgcattttgggtgtataagccatcaata 3051

Query: 2920 ttcagcaaatgattcctttcttt-nnnnnnnnnntgtggaggaaagtagaaatttacc 2978
|||||

Sbjct: 3052 ttcagcaaatgattcctttctttaaaaaaaaaaattgtggaggaaagtagaaatttacc 3111

Query: 2979 aaggttgttggccagggcggttaaattcacagannnnnnnaacgagaaaaacacacagaa 3038
|||||

Sbjct: 3112 aaggttgttggccagggcggttaaattcacagatttttttaacgagaaaaacacacagaa 3171

Query: 3039 gaagctacctcaggtgtttttacctcagcaccttgctcttggtttcccttagagatttt 3098
|||||

Sbjct: 3172 gaagctacctcaggtgtttttacctcagcaccttgctcttggtttcccttagagatttt 3231

Query: 3099 gtaaagctgatagttggagcannnnnnnnnnnnnaataaaaatgagttggnnnnnnnn 3158
|||||

Sbjct: 3232 gtaaagctgatagttggagcattttttttatttttttaataaaaatgagttggaaaaaaaaa 3291

Query: 3159 taagatatcaactgccagcctggagaaggtgacagtccaagtgtgcaacagctgttctga 3218

|||||
Sbjct: 3292 taagatatcaactgccagcctggagaaggtgacagtccaagtgtgcaacagctgttctga 3351

Query: 3219 attgtcttccgctagccaagaaccnatatggccttcttttggacaaaccttgaaaatgtt 3278

|||||
Sbjct: 3352 attgtcttccgctagccaagaacctatatggccttcttttggacaaaccttgaaaatgtt 3411

Query: 3279 tattt 3283

|||||
Sbjct: 3412 tattt 3416

>gi|33878041|gb|BC021290.2| Homo sapiens IGF-II mRNA-binding protein 2, mRNA (cDNA c
MGC:29539 IMAGE:5090334), complete cds
Length = 3633

Score = 2675 bits (1391), Expect = 0.0

Identities = 1406/1421 (98%)

Strand = Plus / Plus

Query: 1141 acccactccggatacttctccagcctgtacccccatcaccagtttgcccggttcccgcat 1200

|||||
Sbjct: 1265 acccactccggatacttctccagcctgtacccccatcaccagtttgcccggttcccgcat 1324

Query: 1201 catcactcttatccagagcaggagattgtgaatctcttcacccaaccaggctgtgggc 1260

|||||
Sbjct: 1325 catcactcttatccagagcaggagattgtgaatctcttcacccaaccaggctgtgggc 1384

Query: 1261 gccatcatcggaagaagggggcacacatcaaacagctggcgagattcgccggagcctct 1320

|||||
Sbjct: 1385 gccatcatcggaagaagggggcacacatcaaacagctggcgagattcgccggagcctct 1444

Query: 1321 atcaagattgcccctgcggaaggccagacgtcagcgaaaggatggtcatcatcaccggg 1380

|||||
Sbjct: 1445 atcaagattgcccctgcggaaggccagacgtcagcgaaaggatggtcatcatcaccggg 1504

Query: 1381 ccaccggaagcccagttcaaggcccaggacggatctttgggaaactgaaagaggaaaac 1440

|||||
Sbjct: 1505 ccaccggaagcccagttcaaggcccaggacggatctttgggaaactgaaagaggaaaac 1564

Query: 1441 ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgcctcttccaca 1500

|||||
Sbjct: 1565 ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgcctcttccaca 1624

Query: 1501 gctggccgggtgattggcaaaggtggcaagaccgtgaacgaactgcagaacttaaccagt 1560

|||||
Sbjct: 1625 gctggccgggtgattggcaaaggtggcaagaccgtgaacgaactgcagaacttaaccagt 1684

Query: 1561 gcagaagtcacgtgcctcgtgaccaaaccgagatgaaaatgaggaagtgatcgtcaga 1620

|||||
Sbjct: 1685 gcagaagtcacgtgcctcgtgaccaaaccgagatgaaaatgaggaagtgatcgtcaga 1744



Your request has been successfully submitted and put into the Blast Queue.

Query = (3283 letters)

The request ID is

or

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ Linkout ☐ Sequence Retrieval ☒ NCBI-gi in

Number of: Descriptions Alignments

Alignment view

Limit results by or select from:
entrez query

Expect value
range:



Your request has been successfully submitted and put into the Blast Queue.

seq

Query = (3283 letters)

The request ID is

or

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi in

Number of: Descriptions Alignments

Alignment view

Start formatting from query #

Limit results by or select from:

Expect value range:

Results file ☐

seq 5 vs patent database

Sequences producing significant alignments:

	Score (bits)	E Value	
gi 17910814 gb AR171864.1 AR171864 Sequence 5 from patent U...	3356	0.0	<i>parent instant</i>
gi 33019694 dbj BD209924.1 Isolated nucleic acid molecules...	3356	0.0	<i>instant</i>
gi 33738475 gb AR343073.1 Sequence 5 from patent US <u>6576756</u>	3356	0.0	<i>instant</i>
gi 17910816 gb AR171866.1 AR171866 Sequence 7 from patent U...	3285	0.0	
gi 33019696 dbj BD209926.1 Isolated nucleic acid molecules...	3285	0.0	
gi 33738477 gb AR343075.1 Sequence 7 from patent US 6576756	3285	0.0	
gi 23222756 dbj BD127811.1 Primer for synthesizing full-le...	2732	0.0	



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 lcl|seq_1 Length 1946 (1 .. 1946)

Sequence 2 gi 4191607 Length 2130 (1 .. 2130)



SEQ 7
gi 4191607

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 3484 bits (1812), Expect = 0.0
 Identities = 1834/1845 (99%), Gaps = 6/1845 (0%)
 Strand = Plus / Plus

```

Query:                108  aggagccggaaaattcaaatccgaaatattccaccccagctccgatggg
                        |||
Sbjct:                244  aggagccggaaaattcaaatccgaaatattccaccccagctccgatggg
IGF-II mRNA-binding protein 1 79  R S R K I Q I R N I P P Q L R W

Query:                168  agcctgctgggtcagtatggtacagtagagaactgtgagcaagtgaaca
                        |||
Sbjct:                304  agcctgctgggtcagtatggtacagtagagaactgtgagcaagtgaaca
IGF-II mRNA-binding protein 1 99  S L L A Q Y G T V E N C E Q V N

Query:                228  acggcagtggtgaatgtcacctattccaaccgggagcagaccagggaag
                        |||
Sbjct:                364  acggcagtggtgaatgtcacctattccaaccgggagcagaccagggaag
IGF-II mRNA-binding protein 1 119 T A V V N V T Y S N R E Q T R Q

Query:                288  ctgaatggccaccagttggagaaccatgccctgaaggtctcctacatcc
                        |||
Sbjct:                424  ctgaatggccaccagttggagaaccatgccctgaaggtctcctacatcc
IGF-II mRNA-binding protein 1 139 L N G H Q L E N H A L K V S Y I
  
```

```
Query:          348  atagcacagggacctgagaatgggcgccgagggggctttggctctcggg
                   |||
Sbjct:          484  atagcacagggacctgagaatgggcgccgagggggctttggctctcggg
IGF-II mRNA-binding protein 1 159  I A Q G P E N G R R G G F G S R

Query:          408  cagggtcacctgtggcagcggggggcccgccaagcagcagcaagtgg
                   |||
Sbjct:          544  cagggtcacctgtggcagcggggggcccgccaagcagcagcaagtgg
IGF-II mRNA-binding protein 1 179  Q G S P V A A G A P A K Q Q Q V

Query:          468  cggctcctgggtgccaccagtatgtgggtgccattattggcaaggagg
                   |||
Sbjct:          604  cggctcctgggtgccaccagtatgtgggtgccattattggcaaggagg
IGF-II mRNA-binding protein 1 199  R L L V P T Q Y V G A I I G K E

Query:          528  cgcaacatcacaaaacagaccagtcgaagatagacgtgcataggaagg
                   |||
Sbjct:          664  cgcaacatcacaaaacagaccagtcgaagatagacgtgcataggaagg
IGF-II mRNA-binding protein 1 219  R N I T K Q T Q S K I D V H R K

Query:          588  gcagctgaaaaagccatcagtgctgactccaccctgagggctgctcct
                   |||
Sbjct:          724  gcagctgaaaaagccatcagtgctgactccaccctgagggctgctcct
IGF-II mRNA-binding protein 1 239  A A E K A I S V H S T P E G C S

Query:          648  atgatcttgagattatgcataaagaggctaaggacaccaaaccggctg
                   |||
Sbjct:          784  atgatcttgagattatgcataaagaggctaaggacaccaaaccggctg
IGF-II mRNA-binding protein 1 259  M I L E I M H K E A K D T K T A

Query:          708  ctgaagatcctggcccataataactttgtaggcgctctcattggcaagg
                   |||
Sbjct:          844  ctgaagatcctggcccataataactttgtaggcgctctcattggcaagg
IGF-II mRNA-binding protein 1 279  L K I L A H N N F V G R L I G K

Query:          768  ctgaagaaggtagagcaagataccgagacaaaaatcaccatctcctcgt
                   |||
Sbjct:          904  ctgaagaaggtagagcaagataccgagacaaaaatcaccatctcctcgt
IGF-II mRNA-binding protein 1 299  L K K V E Q D T E T K I T I S S

Query:          828  accctttacaaccctgagaggaccatcactgtgaagggggccatcgaga
                   |||
Sbjct:          964  accctttacaaccctgagaggaccatcactgtgaagggggccatcgaga
IGF-II mRNA-binding protein 1 319  T L Y N P E R T I T V K G A I E

Query:          888  gccgagcaggaaataatgaagaaagtgcgggaggcctatgagaatgatg
                   |||
Sbjct:          1024 gccgagcaggaaataatgaagaaagtgcgggaggcctatgagaatgatg
IGF-II mRNA-binding protein 1 339  A E Q E I M K K V R E A Y E N D

Query:          948  agc-----tctcacctgatccctggcctgaacctggctgctgtaggtc
                   |||
Sbjct:          1084 agcctgcagtctcacctgatccctggcctgaacctggctgctgtaggtc
```

IGF-II mRNA-binding protein 1 359 S L Q S H L I P G L N L A A V G

Query: 1002 tcatccagcgcagtcctccgcccctccagcagcgttactggggctgctc
Sbjct: 1144 tcatccagcgcagtcctccgcccctccagcagcgttactggggctgctc
IGF-II mRNA-binding protein 1 379 S S S A V P P P S S V T G A A

Query: 1062 tttatgcaggctcccgagcaggagatgggtgcagggtgtttatccccgccc
Sbjct: 1204 tttatgcaggctcccgagcaggagatgggtgcagggtgtttatccccgccc
IGF-II mRNA-binding protein 1 399 F M Q A P E Q E M V Q V F I P A

Query: 1122 gccatcatcggaagaagggcagcacatcaaacagctctccccggtttg
Sbjct: 1264 gccatcatcggaagaagggcagcacatcaaacagctctccccggtttg
IGF-II mRNA-binding protein 1 419 A I I G K K G Q H I K Q L S R F

Query: 1182 atcaagattgcaccacccgaaacacctgactccaaagttcgtatggtta
Sbjct: 1324 atcaagattgcaccacccgaaacacctgactccaaagttcgtatggtta
IGF-II mRNA-binding protein 1 439 I K I A P P E T P D S K V R M V

Query: 1242 ccgccagaggcccaattcaaggctcaggaagaatctatggcaaactca
Sbjct: 1384 ccgccagaggcccaattcaaggctcaggaagaatctatggcaaactca
IGF-II mRNA-binding protein 1 459 P P E A Q F K A Q G R I Y G K L

Query: 1302 ttctttggtcccaaggaggaagtgaagctggagaccacatacgtgtgc
Sbjct: 1444 ttctttggtcccaaggaggaagtgaagctggagaccacatacgtgtgc
IGF-II mRNA-binding protein 1 479 F F G P K E E V K L E T H I R V

Query: 1362 gctggccgggtcattggcaaaggtggaaaaacggtgaacgagttgcaga
Sbjct: 1504 gctggccgggtcattggcaaaggtggaaaaacggtgaacgagttgcaga
IGF-II mRNA-binding protein 1 499 A G R V I G K G G K T V N E L Q

Query: 1422 gctgaggtggtagtaccaagagaccagaccctgatgagaacgaccagg
Sbjct: 1564 gctgaggtggtagtaccaagagaccagaccctgatgagaacgaccagg
IGF-II mRNA-binding protein 1 519 A E V V V P R D Q T P D E N D Q

Query: 1482 atcatcggacatttctatgccagtcagatgggtcaacggaagatccgag
Sbjct: 1624 atcatcggacatttctatgccagtcagatgggtcaacggaagatccgag
IGF-II mRNA-binding protein 1 539 I I G H F Y A S Q M A Q R K I R

Query: 1542 caggttaagcagcagcatcagaagggacagagtaaccaggcccaggcac
Sbjct: 1684 caggttaagcagcagcatcagaagggacagagtaaccaggcccaggcac
IGF-II mRNA-binding protein 1 559 Q V K Q Q H Q K G Q S N Q A Q A

Query: 1602 ccagccctccctgtcccttngagtccaggacaacaacgggcagaaatc
Sbjct: 1744 ccagccctccctgtcccttngagtccaggacaacaacgggcagaaatc

```
Sbjct:          1744 ccagccctccctgtcccttcgagtcaggacaacaacgggcagaaatc

Query:          1662 ctccccggcaggcctgagaatgagtgggaatccgggacacntgggccgg
                  |||
Sbjct:          1804 ctccccggcaggcctgagaatgagtgggaatccgggacacctgggccgg

Query:          1722 ggtttgccacttgattgagaaagatgttcagtgaggaaccctgatct
                  |||
Sbjct:          1864 ggtttgccacttgattgagaaagatgttcagtgaggaaccctgatct

Query:          1782 acacccacccaattggcccaacactgtntgccctcgggggtgtcagaaa
                  |||
Sbjct:          1924 acacccacccaattggcccaacactgtctgccctcgggggtgtcagaaa

Query:          1842 ggcacttttaaacgtggattgtttaagaagctctccaggccccaccaa
                  |||
Sbjct:          1984 ggcacttttaaacgtggattgtttaagaagctctccaggccccaccaa

Query:          1902 acacctcagtggggaagaaaaataaaatttccttcagggttttaaaa 194
                  |||
Sbjct:          2044 acacctcagtggggaagaaaaataaaatttccttcagggttttaaaa 208
```

CPU time: 0.04 user secs. 0.00 sys. secs 0.04 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 13
Number of Sequences: 0
Number of extensions: 13
Number of successful extensions: 2
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 1946
length of database: 8,918,056,233
effective HSP length: 25
effective length of query: 1921
effective length of database: 8,918,056,208
effective search space: 17131585975568
effective search space used: 17131585975568
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

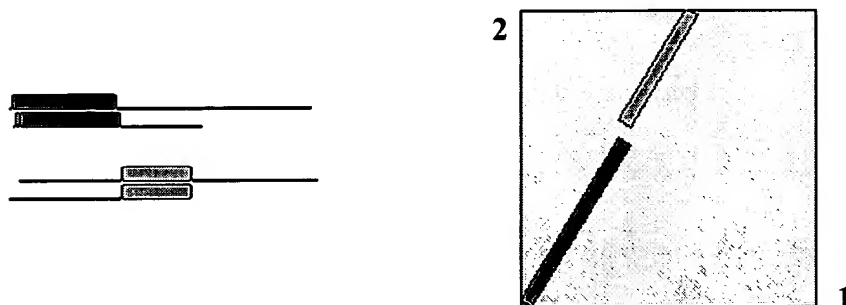
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

SE8
4/19/609

Sequence 1 lcl|seq_1 Length 3283 (1 .. 3283)

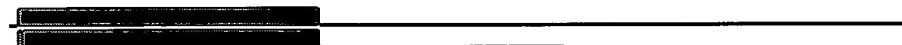
Sequence 2 gi 4191609 Length 2010 (1 .. 2010)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 2090 bits (1087), Expect = 0.0
 Identities = 1098/1101 (99%), Gaps = 1/1101 (0%)
 Strand = Plus / Plus



Query: 40 gggagccgcgggctctcggggaagagacggatgatgaacaagctttaca
 |||||
 Sbjct: 18 gggagccgcggcctca-ggggaagagacggatgatgaacaagctttaca
 IGF-II mRNA-binding protein 2 1 M N K L Y

Query: 100 agccccgcgcgtcaccgcccagacctccggcagctctttggggacagga
 |||||
 Sbjct: 77 agccccgcgcgtcaccgcccagacctccggcagctctttggggacagga
 IGF-II mRNA-binding protein 2 10 S P A V T A D D L R Q L F G D R

Query: 160 gcgggacaggtcctgctgaagtccggctacgccttcgtggactaccccg
 |||||
 Sbjct: 137 gcgggacaggtcctgctgaagtccggctacgccttcgtggactaccccg
 IGF-II mRNA-binding protein 2 30 A G Q V L L K S G Y A F V D Y P

Query: 220 gccatccgcgccatcgagaccctctcgggtaaagtggaattgcatggga
 |||||
 Sbjct: 197 gccatccgcgccatcgagaccctctcgggtaaagtggaattgcatggga
 IGF-II mRNA-binding protein 2 50 A I R A I E T L S G K V E L H G

```
Query:                280  gttgattactcagtcctctaaaaagctaaggagcaggaaaattcagattc
                        |||
Sbjct:                257  gttgattactcagtcctctaaaaagctaaggagcaggaaaattcagattc
IGF-II mRNA-binding protein 2 70  V D Y S V S K K L R S R K I Q I

Query:                340  cctcacctgcagtgagggtgttggatggacttttggctcaatatggga
                        |||
Sbjct:                317  cctcacctgcagtgagggtgttggatggacttttggctcaatatggga
IGF-II mRNA-binding protein 2 90  P H L Q W E V L D G L L A Q Y G

Query:                400  gtggaacaagtcaacacagacacagaaaccgccgttgtcaacgtcacat
                        |||
Sbjct:                377  gtggaacaagtcaacacagacacagaaaccgccgttgtcaacgtcacat
IGF-II mRNA-binding protein 2 110 V E Q V N T D T E T A V V N V T

Query:                460  gaagaagcaaaaatagccatggagaagctaagcgggcatcagtttgaga
                        |||
Sbjct:                437  gaagaagcaaaaatagccatggagaagctaagcgggcatcagtttgaga
IGF-II mRNA-binding protein 2 130 E E A K I A M E K L S G H Q F E

Query:                520  aagatttcctacatcccggatgaagaggtgagctccccttcgccccctc
                        |||
Sbjct:                497  aagatttcctacatcccggatgaagaggtgagctccccttcgccccctc
IGF-II mRNA-binding protein 2 150 K I S Y I P D E E V S S P S P P

Query:                580  cgtggggaccactcttcccgggagcaaggccacgcccctgggggcactt
                        |||
Sbjct:                557  cgtggggaccactcttcccgggagcaaggccacgcccctgggggcactt
IGF-II mRNA-binding protein 2 170 R G D H S S R E Q G H A P G G T

Query:                640  cagattgatttcccgtgcggatcctgggtccccaccagtttggttggtg
                        |||
Sbjct:                617  cagattgatttcccgtgcggatcctgggtccccaccagtttggttggtg
IGF-II mRNA-binding protein 2 190 Q I D F P L R I L V P T Q F V G

Query:                700  aaggagggccttgaccataaagaacatcactaagcagaccagtcgccggg
                        |||
Sbjct:                677  aaggagggccttgaccataaagaacatcactaagcagaccagtcgccggg
IGF-II mRNA-binding protein 2 210 K E G L T I K N I T K Q T Q S R

Query:                760  agaaaagagaactctggagctgcagagaagcctgtcaccatccatgcc
                        |||
Sbjct:                737  agaaaagagaactctggagctgcagagaagcctgtcaccatccatgcc
IGF-II mRNA-binding protein 2 230 R K E N S G A A E K P V T I H A

Query:                820  acttctgaagcatgccgcatgattccttgaaatcatgcagaaagaggcag
                        |||
Sbjct:                797  acttctgaagcatgccgcatgattccttgaaatcatgcagaaagaggcag
IGF-II mRNA-binding protein 2 250 T S E A C R M I L E I M Q K E A

Query:                880  ctagccgaagagattcctctgaaaatcctggcacacaatggcttggttg
                        |||
Sbjct:                857  ctagccgaagagattcctctgaaaatcctggcacacaatggcttggttg
```

IGF-II mRNA-binding protein 2 270 L A E E I P L K I L A H N G L V

Query: 940 ggaaaagaaggcagaaatttgaagaaaattgaacatgaaacagggacca
Sbjct: 917 ggaaaagaaggcagaaatttgaagaaaattgaacatgaaacagggacca
IGF-II mRNA-binding protein 2 290 G K E G R N L K K I E H E T G T

Query: 1000 tcatctttgcaggatttgagcatatacaaccggaagaaccatcactg
Sbjct: 977 tcatctttgcaggatttgagcatatacaaccggaagaaccatcactg
IGF-II mRNA-binding protein 2 310 S S L Q D L S I Y N P E R T I T

Query: 1060 gttgaggcctgtgccagtgtgagatagagattatgaagaagctgcgtg
Sbjct: 1037 gttgaggcctgtgccagtgtgagatagagattatgaagaagctgcgtg
IGF-II mRNA-binding protein 2 330 V E A C A S A E I E I M K K L R

Query: 1120 aatgatatgctggctgtaac 1140
Sbjct: 1097 aatgatatgctggctgtaac 1117
IGF-II mRNA-binding protein 2 350 N D M L A V N

Score = 1469 bits (764), Expect = 0.0
Identities = 764/764 (100%)
Strand = Plus / Plus

Query: 1141 acccactccggatacttctccagcctgtacccccatcaccagtttggcc
Sbjct: 1247 acccactccggatacttctccagcctgtacccccatcaccagtttggcc
IGF-II mRNA-binding protein 2 400 T H S G Y F S S L Y P H H Q F G

Query: 1201 catcactcttatccagagcaggagattgtgaatctcttcacccaaccc
Sbjct: 1307 catcactcttatccagagcaggagattgtgaatctcttcacccaaccc
IGF-II mRNA-binding protein 2 420 H H S Y P E Q E I V N L F I P T

Query: 1261 gccatcatcggaagaagggggcacacatcaaacagctggcgagattcg
Sbjct: 1367 gccatcatcggaagaagggggcacacatcaaacagctggcgagattcg
IGF-II mRNA-binding protein 2 440 A I I G K K G A H I K Q L A R F

Query: 1321 atcaagattgcccctgcggaaggcccagacgtcagcgaaaggatgggtca
Sbjct: 1427 atcaagattgcccctgcggaaggcccagacgtcagcgaaaggatgggtca
IGF-II mRNA-binding protein 2 460 I K I A P A E G P D V S E R M V

Query: 1381 ccaccggaagcccagttcaaggcccagggacggatctttgggaaactga
Sbjct: 1487 ccaccggaagcccagttcaaggcccagggacggatctttgggaaactga
IGF-II mRNA-binding protein 2 480 P P E A Q F K A Q G R I F G K L

Query: 1441 ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgc
Sbjct: 1547 ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgc

```

Sbjct:                               1547 ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtg
IGF-II mRNA-binding protein 2 500   F F N P K E E V K L E A H I R V

Query:                               1501 gctggccgggtgattggcaaaggtggcaagaccgtgaacgaactgcaga
                               |||||
Sbjct:                               1607 gctggccgggtgattggcaaaggtggcaagaccgtgaacgaactgcaga
IGF-II mRNA-binding protein 2 520   A G R V I G K G G K T V N E L Q

Query:                               1561 gcagaagtcatcgtgcctcgtgaccaaacgccagatgaaaatgaggaag
                               |||||
Sbjct:                               1667 gcagaagtcatcgtgcctcgtgaccaaacgccagatgaaaatgaggaag
IGF-II mRNA-binding protein 2 540   A E V I V P R D Q T P D E N E E

Query:                               1621 attatcgggcacttctttgctagccagactgcacagcgcaagatcaggg
                               |||||
Sbjct:                               1727 attatcgggcacttctttgctagccagactgcacagcgcaagatcaggg
IGF-II mRNA-binding protein 2 560   I I G H F F A S Q T A Q R K I R

Query:                               1681 caggtgaagcagcaggagcagaaataccctcagggagtcgcctcacagc
                               |||||
Sbjct:                               1787 caggtgaagcagcaggagcagaaataccctcagggagtcgcctcacagc
IGF-II mRNA-binding protein 2 580   Q V K Q Q E Q K Y P Q G V A S Q

Query:                               1741 ggctcccacaggcaccagcaaaacaacggatgaatgtagcccttccaac
                               |||||
Sbjct:                               1847 ggctcccacaggcaccagcaaaacaacggatgaatgtagcccttccaac

Query:                               1801 tgagaccaaacgcagccagccagatcgggagcaaaccaaagaccatctg
                               |||||
Sbjct:                               1907 tgagaccaaacgcagccagccagatcgggagcaaaccaaagaccatctg

Query:                               1861 gtctgcggaggcgccagggactctgccgaggccctgagaaccc 1904
                               |||||
Sbjct:                               1967 gtctgcggaggcgccagggactctgccgaggccctgagaaccc 2010

CPU time:      0.04 user secs.      0.01 sys. secs      0.05 total secs.

Lambda      K      H
1.33      0.621      1.12

Gapped
Lambda      K      H
1.33      0.621      1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 9
Number of Sequences: 0
Number of extensions: 9
Number of successful extensions: 4
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 4
length of query: 3283
length of database: 8,918,056,233

```

effective HSP length: 26
effective length of query: 3257
effective length of database: 8,918,056,207
effective search space: 29046109066199
effective search space used: 29046109066199
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 22 (43.0 bits)

 **NCBI**
Nucleotide Protein Translations Retrieve results for an RID

formatting **BLAST**

Your request has been successfully submitted and put into the Blast Queue.

Query = (556 letters)

The request ID is 1061925537-609-1058353.BLASTQ3

p62 in
pat
database

Format! or **Reset all**

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi Alignment ☐ in HTML

Number of: Descriptions 100 Alignments 50

Alignment view Pairwise

Format for PSI-BLAST ☐ with inclusion threshold: 0.005

Limit results by or select from: (none)

Expect value
range:



results of BLAST

BLASTN 2.2.6 [Apr-09-2003]

RID: 1061916244-523-2727514.BLASTQ3

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)

1,886,208 sequences; 8,918,056,233 total letters

Taxonomy reports

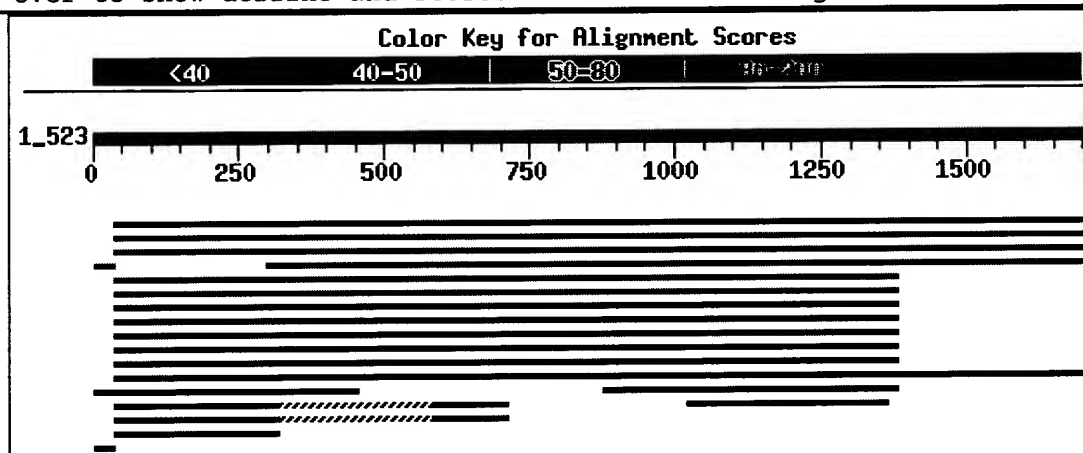
Query=

(1708 letters)

SEQ 5

Distribution of 33 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score E
(bits) Value

gi	4191607	gb	AF117106.1	AF117106	Homo sapiens IGF-II mRNA...	3167	0.0
gi	21361351	ref	NM 006546.2		Homo sapiens IGF-II mRNA-bindi...	3130	0.0
gi	7141071	gb	AF198254.1	AF198254	Homo sapiens mRNA-binding...	3130	0.0
gi	22760672	dbj	AK074915.1		Homo sapiens cDNA FLJ90434 fis,...	2663	0.0
gi	31342209	ref	NM 175594.2		Rattus norvegicus IGF-II mRNA...	1727	0.0
gi	27464837	gb	AF541940.1		Rattus norvegicus b-actin zipcod...	1727	0.0
gi	31560605	ref	NM 009951.2		Mus musculus insulin-like grow...	1675	0.0
gi	12851513	dbj	AK013940.1		Mus musculus 13 days embryo hea...	1675	0.0
gi	3273748	gb	AF061569.1	AF061569	Mus musculus coding regio...	1675	0.0
gi	26336870	dbj	AK044850.1		Mus musculus 9.5 days embryo pa...	1669	0.0
gi	30354043	gb	BC051679.1		Mus musculus insulin-like growth...	1669	0.0
gi	24580458	gb	AC105030.11		Homo sapiens chromosome 17, clo...	829	0.0
gi	21637524	gb	AC091133.11		Homo sapiens chromosome 17, clo...	546	e-152
gi	30581644	gb	AC094527.7		Rattus norvegicus 5 BAC CH230-4L...	477	e-131
gi	27689046	ref	XM 220886.1		Rattus norvegicus similar to I...	477	e-131
gi	22204252	emb	AL606704.20		Mouse DNA sequence from clone ...	344	2e-91
gi	21954991	gb	AC098642.5		Genomic sequence for Mus musculu...	344	2e-91
gi	14475918	gb	AC084407.10		Mus Musculus Strain C57BL6/J Ch...	344	2e-91

gi 15878883 emb AJ334465.1 HSA334465	Homo sapiens genomic s...	70	1e-08
gi 15876265 emb AJ331847.1 HSA331847	Homo sapiens genomic s...	70	1e-08

Alignments

>gi|4191607|gb|AF117106.1|AF117106 Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1)
Length = 2130

Score = 3167 bits (1647), Expect = 0.0
Identities = 1667/1678 (99%), Gaps = 6/1678 (0%)
Strand = Plus / Plus

Query: 37 agccatcatgaagctgaatggccaccagttggagaaccatgccctgaaggtctcctacat 96
|||
Sbjct: 411 agccatcatgaagctgaatggccaccagttggagaaccatgccctgaaggtctcctacat 470

Query: 97 ccccgatgagcagatagcacaggacctgagaatggcgccgaggggctttggctctcg 156
|||
Sbjct: 471 ccccgatgagcagatagcacaggacctgagaatggcgccgaggggctttggctctcg 530

Query: 157 gggtcagccccgccagggtcacctgtggcagcggggccccagccaagcagcagcaagt 216
|||
Sbjct: 531 gggtcagccccgccagggtcacctgtggcagcggggccccagccaagcagcagcaagt 590

Query: 217 ggacatcccccttcggctcctggtgccaccagtatgtgggtgccattattggcaagga 276
|||
Sbjct: 591 ggacatcccccttcggctcctggtgccaccagtatgtgggtgccattattggcaagga 650

Query: 277 gggggccaccatccgcaacatcacaaaacagaccagtcgaagatagacgtgcataggaa 336
|||
Sbjct: 651 gggggccaccatccgcaacatcacaaaacagaccagtcgaagatagacgtgcataggaa 710

Query: 337 ggagaacgcaggtgcagctgaaaaagccatcagtgtgcactccaccctgagggctgctc 396
|||
Sbjct: 711 ggagaacgcaggtgcagctgaaaaagccatcagtgtgcactccaccctgagggctgctc 770

Query: 397 ctccgcttgtaagatgatcttgagattatgcataaagaggctaaggacacaaaacggc 456
|||
Sbjct: 771 ctccgcttgtaagatgatcttgagattatgcataaagaggctaaggacacaaaacggc 830

Query: 457 tgacgaggttcccctgaagatcctggcccataataactttgtagggcgtctcattggcaa 516
|||
Sbjct: 831 tgacgaggttcccctgaagatcctggcccataataactttgtagggcgtctcattggcaa 890

Query: 517 ggaaggacggaacctgaagaaggtagagcaagataccgagacaaaaatcaccatctcctc 576
|||
Sbjct: 891 ggaaggacggaacctgaagaaggtagagcaagataccgagacaaaaatcaccatctcctc 950

Query: 577 gttgcaagaccttaccctttacaaccctgagaggaccatcactgtgaagggggccatcga 636
|||
Sbjct: 951 gttgcaagaccttaccctttacaaccctgagaggaccatcactgtgaagggggccatcga 1010

Query: 637 gaattgttgaggccgagcaggaaataatgaagaaagttcgggaggcctatgagaatga 696
|||

 **NCBI**
Nucleotide Protein Translations Retrieve results for an RID

formatting **BLAST**

Your request has been successfully submitted and put into the Blast Queue.

Query = (1708 letters)

*megablast
SEQ 5*

The request ID is

Format! or **Reset all**

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi in

Number of: Descriptions Alignments

Alignment view

Start formatting
from query #

Limit results by or select from:

Expect value
range:

Results file ☐



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

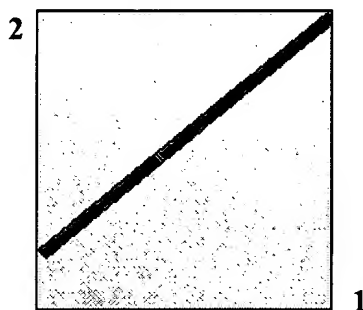
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 lcl|seq_1 Length 1708 (1 .. 1708)

Sequence 2 gi 4191607 Length 2130 (1 .. 2130)

seq 5
4191607



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 3163 bits (1645), Expect = 0.0
 Identities = 1667/1678 (99%), Gaps = 6/1678 (0%)
 Strand = Plus / Plus

```
Query:          37  agccatcatgaagctgaatggccaccagttggagaacctatgcctgaag
                  |||
Sbjct:          411  agccatcatgaagctgaatggccaccagttggagaacctatgcctgaag
IGF-II mRNA-binding protein 1 135  A I M K L N G H Q L E N H A L K
```

```
Query:          97  ccccgatgagcagatagcacaggacctgagaatggcgccgagggggc
                  |||
Sbjct:          471  ccccgatgagcagatagcacaggacctgagaatggcgccgagggggc
IGF-II mRNA-binding protein 1 155  P D E Q I A Q G P E N G R R G G
```

```
Query:          157  gggtcagccccgccagggtcacctgtggcagcgggggccccagccaag
                  |||
Sbjct:          531  gggtcagccccgccagggtcacctgtggcagcgggggccccagccaag
IGF-II mRNA-binding protein 1 175  G Q P R Q G S P V A A G A P A K
```

```
Query:          217  ggacatcccccttcggctcctggtgccaccagtatgtgggtgccatt
                  |||
Sbjct:          591  ggacatcccccttcggctcctggtgccaccagtatgtgggtgccatt
IGF-II mRNA-binding protein 1 195  D I P L R L L V P T Q Y V G A I
```

```
Query:          277  gggggccaccatccgcaacatcacaaaacagacccagtccaagatagac
                   |||
Sbjct:          651  gggggccaccatccgcaacatcacaaaacagacccagtccaagatagac
IGF-II mRNA-binding protein 1 215  G A T I R N I T K Q T Q S K I D

Query:          337  ggagaacgcaggtgcagctgaaaaagccatcagtgtgcactccaccct
                   |||
Sbjct:          711  ggagaacgcaggtgcagctgaaaaagccatcagtgtgcactccaccct
IGF-II mRNA-binding protein 1 235  E N A G A A E K A I S V H S T P

Query:          397  ctccgcttgtaagatgatcttggagattatgcataaagaggctaaggac
                   |||
Sbjct:          771  ctccgcttgtaagatgatcttggagattatgcataaagaggctaaggac
IGF-II mRNA-binding protein 1 255  S A C K M I L E I M H K E A K D

Query:          457  tgacgaggttccccctgaagatcctggcccataataactttgtagggcgt
                   |||
Sbjct:          831  tgacgaggttccccctgaagatcctggcccataataactttgtagggcgt
IGF-II mRNA-binding protein 1 275  D E V P L K I L A H N N F V G R

Query:          517  ggaaggacggaacctgaagaaggtagagcaagataccgagacaaaaatc
                   |||
Sbjct:          891  ggaaggacggaacctgaagaaggtagagcaagataccgagacaaaaatc
IGF-II mRNA-binding protein 1 295  E G R N L K K V E Q D T E T K I

Query:          577  gttgcaagaccttaccctttacaaccctgagaggaccatcactgtgaag
                   |||
Sbjct:          951  gttgcaagaccttaccctttacaaccctgagaggaccatcactgtgaag
IGF-II mRNA-binding protein 1 315  L Q D L T L Y N P E R T I T V K

Query:          637  gaattgttgcaaggccgagcaggaaataatgaagaaagttcgggaggcc
                   |||
Sbjct:          1011  gaattgttgcaaggccgagcaggaaataatgaagaaagttcgggaggcc
IGF-II mRNA-binding protein 1 335  N C C R A E Q E I M K K V R E A

Query:          697  tgtggctgcatgagc-----tctcacctgatccctggcctgaacctg
                   |||
Sbjct:          1071  tgtggctgcatgagcctgcagtctcacctgatccctggcctgaacctg
IGF-II mRNA-binding protein 1 355  V A A M S L Q S H L I P G L N L

Query:          751  tcttttccagcttcatccagcgcagtcctcgccgctccagcagcggtt
                   |||
Sbjct:          1131  tcttttccagcttcatccagcgcagtcctcgccgctccagcagcggtt
IGF-II mRNA-binding protein 1 375  L F P A S S S A V P P P P S S V

Query:          811  tccctatagctcctttatgcaggctcccagcaggagatggtgcaggtg
                   |||
Sbjct:          1191  tccctatagctcctttatgcaggctcccagcaggagatggtgcaggtg
IGF-II mRNA-binding protein 1 395  P Y S S F M Q A P E Q E M V Q V

Query:          871  ccaggcagtgggcgccatcatcggcaagaaggggcagcacatcaaacag
                   |||
Sbjct:          1251  ccaggcagtgggcgccatcatcggcaagaaggggcagcacatcaaacag
```

IGF-II mRNA-binding protein 1 415 Q A V G A I I G K K G Q H I K Q

Query: 931 tgccagcgcctccatcaagattgcaccacccgaaacacctgactccaaa
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 1311 tgccagcgcctccatcaagattgcaccacccgaaacacctgactccaaa
IGF-II mRNA-binding protein 1 435 A S A S I K I A P P E T P D S K

Query: 991 tatcatcactggaccgccagaggccaattcaaggctcaggaagaatc
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 1371 tatcatcactggaccgccagaggccaattcaaggctcaggaagaatc
IGF-II mRNA-binding protein 1 455 I I T G P P E A Q F K A Q G R I

Query: 1051 caaggaggagaacttctttgggtcccaaggaggaagtgaagctggagacc
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 1431 caaggaggagaacttctttgggtcccaaggaggaagtgaagctggagacc
IGF-II mRNA-binding protein 1 475 K E E N F F G P K E E V K L E T

Query: 1111 gccagcatcagcagctggccgggtcattggcaaagggtggaaaaacggtg
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 1491 gccagcatcagcagctggccgggtcattggcaaagggtggaaaaacggtg
IGF-II mRNA-binding protein 1 495 P A S A A G R V I G K G G K T V

Query: 1171 gaatttgacggcagctgaggtggtagtaccaagagaccagaccctgat
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 1551 gaatttgacggcagctgaggtggtagtaccaagagaccagaccctgat
IGF-II mRNA-binding protein 1 515 N L T A A E V V V P R D Q T P D

Query: 1231 ggtcatcgtagaaaatcatcggacatttctatgccagtcagatgggtcaa
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 1611 ggtcatcgtagaaaatcatcggacatttctatgccagtcagatgggtcaa
IGF-II mRNA-binding protein 1 535 V I V K I I G H F Y A S Q M A Q

Query: 1291 agacatcctggcccagggttaagcagcagcatcagaagggacagagtaac
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 1671 agacatcctggcccagggttaagcagcagcatcagaagggacagagtaac
IGF-II mRNA-binding protein 1 555 D I L A Q V K Q Q H Q K G Q S N

Query: 1351 acggaggaagtgaccagccccctccctgtcccttnagatccaggacaaca
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 1731 acggaggaagtgaccagccccctccctgtcccttcgagatccaggacaaca
IGF-II mRNA-binding protein 1 575 R R K ^^^

Query: 1411 tcgagagtgtgctctccccggcaggcctgagaatgagtgggaatccggg
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 1791 tcgagagtgtgctctccccggcaggcctgagaatgagtgggaatccggg

Query: 1471 gggctgtagatcaggtttgcccaacttgattgagaaagatgttccagtga
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 1851 gggctgtagatcaggtttgcccaacttgattgagaaagatgttccagtga

Query: 1531 ctntcagccccaaacacccaccaattggcccaacactgtntgccctc
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 1911 ctctcagccccaaacacccaccaattggcccaacactgtctgccctc

Query: 1591 aattntagcgcaaggcactttttaacgtggattgtttaagaagctctc
||| ||||||||||||||||||||||||||||||||||||||||
Sbjct: 1971 aattctagcgcaaggcactttttaacgtggattgtttaagaagctctc

Query: 1651 aagaggggtggatcacacctcagtgggaagaaaaataaaatttccttcag
||||||||||||||||||||||||||||||||||||||
Sbjct: 2031 aagaggggtggatcacacctcagtgggaagaaaaataaaatttccttcag

CPU time: 0.00 user secs. 0.02 sys. secs 0.02 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 12
Number of Sequences: 0
Number of extensions: 12
Number of successful extensions: 2
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 1708
length of database: 8,918,056,233
effective HSP length: 25
effective length of query: 1683
effective length of database: 8,918,056,208
effective search space: 15009088598064
effective search space used: 15009088598064
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

● MIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

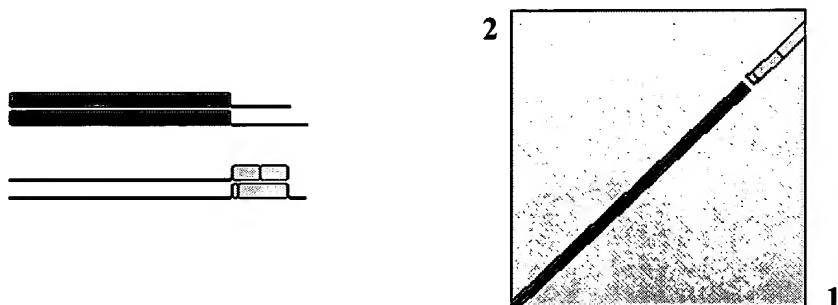
Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 lcl|seq_1

Length 3412 (1 .. 3412)

Sequence 2 gi 27552765 Homo sapiens IGF-II mRNA-binding protein 2
 (IMP-2), mRNA

Length 3642 (1 .. 3642)



SEQ 6
 gi 27552765

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 5107 bits (2656), Expect = 0.0
 Identities = 2671/2686 (99%)
 Strand = Plus / Plus



```

Query:                5      gcggaggagggcaggagcgccgggtaccgggcccggggagccgcgggct
                        |||
Sbjct:                9      gcggaggagggcaggagcgccgggtaccgggcccggggagccgcgggct

Query:               65      gacggatgatgaacaagctttacatcgggaaacctgagccccgccgtcac
                        |||
Sbjct:               69      gacggatgatgaacaagctttacatcgggaaacctgagccccgccgtcac
IGF-II mRNA-binding protein 2 1      M N K L Y I G N L S P A V T

Query:               125     tccggcagctctttggggacaggaagctgccctggcgggacaggtcct
                        |||
Sbjct:               129     tccggcagctctttggggacaggaagctgccctggcgggacaggtcct
IGF-II mRNA-binding protein 2 18     L R Q L F G D R K L P L A G Q V L

Query:               185     gctacgccttcgtggactacccgaccagaactgggccatccgcgccat
                        |||
Sbjct:               189     gctacgccttcgtggactacccgaccagaactgggccatccgcgccat
  
```

IGF-II mRNA-binding protein 2	38	G	Y	A	F	V	D	Y	P	D	Q	N	W	A	I	R	A	I
Query:	245	cgggtaaagtggaattgcatgggaaaatcatggaagttgattactcagt																
Sbjct:	249	cgggtaaagtggaattgcatgggaaaatcatggaagttgattactcagt																
IGF-II mRNA-binding protein 2	58	S	G	K	V	E	L	H	G	K	I	M	E	V	D	Y	S	V
Query:	305	taaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtg																
Sbjct:	309	taaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtg																
IGF-II mRNA-binding protein 2	78	L	R	S	R	K	I	Q	I	R	N	I	P	P	H	L	Q	W
Query:	365	atggacttttggtcaatatgggacagtgaggagaatgtggaacaagtcaa																
Sbjct:	369	atggacttttggtcaatatgggacagtgaggagaatgtggaacaagtcaa																
IGF-II mRNA-binding protein 2	98	D	G	L	L	A	Q	Y	G	T	V	E	N	V	E	Q	V	N
Query:	425	aaaccgcggttgtcaacgtcacatatgcaacaagagaagaagcaaaaat																
Sbjct:	429	aaaccgcggttgtcaacgtcacatatgcaacaagagaagaagcaaaaat																
IGF-II mRNA-binding protein 2	118	E	T	A	V	V	N	V	T	Y	A	T	R	E	E	A	K	I
Query:	485	agctaagcgggcatcagtttgagaactactccttcaagatttcctacat																
Sbjct:	489	agctaagcgggcatcagtttgagaactactccttcaagatttcctacat																
IGF-II mRNA-binding protein 2	138	K	L	S	G	H	Q	F	E	N	Y	S	F	K	I	S	Y	I
Query:	545	aggtgagctcccttcgccccctcagcgagcccagcgtggggaccactc																
Sbjct:	549	aggtgagctcccttcgccccctcagcgagcccagcgtggggaccactc																
IGF-II mRNA-binding protein 2	158	E	V	S	S	P	S	P	P	Q	R	A	Q	R	G	D	H	S
Query:	605	aaggccacgcccctgggggcacttctcaggccagacagattgatttccc																
Sbjct:	609	aaggccacgcccctgggggcacttctcaggccagacagattgatttccc																
IGF-II mRNA-binding protein 2	178	Q	G	H	A	P	G	G	T	S	Q	A	R	Q	I	D	F	P
Query:	665	tggtccccacccagtttggttggtgccatcatcgaaaggagggccttgac																
Sbjct:	669	tggtccccacccagtttggttggtgccatcatcgaaaggagggccttgac																
IGF-II mRNA-binding protein 2	198	L	V	P	T	Q	F	V	G	A	I	I	G	K	E	G	L	T
Query:	725	tcactaagcagacccagtcgccgggtagatatccatagaaaagagaactc																
Sbjct:	729	tcactaagcagacccagtcgccgggtagatatccatagaaaagagaactc																
IGF-II mRNA-binding protein 2	218	I	T	K	Q	T	Q	S	R	V	D	I	H	R	K	E	N	S
Query:	785	agaagcctgtcaccatccatgccaccccagaggggacttctgaagcatg																
Sbjct:	789	agaagcctgtcaccatccatgccaccccagaggggacttctgaagcatg																
IGF-II mRNA-binding protein 2	238	E	K	P	V	T	I	H	A	T	P	E	G	T	S	E	A	C
Query:	845	ttgaaatcatgcagaaagaggcagatgagaccaaactagccgaagagat																

Sbjct:	849	ttgaaatcatgcagaaagaggcagatgagaccaaactagccgaagagat
IGF-II mRNA-binding protein 2	258	L E I M Q K E A D E T K L A E E I
Query:	905	tcttggcacacaatggcttgggttgaagactgattggaaaagaaggcag
Sbjct:	909	tcttggcacacaatggcttgggttgaagactgattggaaaagaaggcag
IGF-II mRNA-binding protein 2	278	I L A H N G L V G R L I G K E G R
Query:	965	aaattgaacatgaaacagggaccaagataacaatctcatctttgcagga
Sbjct:	969	aaattgaacatgaaacagggaccaagataacaatctcatctttgcagga
IGF-II mRNA-binding protein 2	298	K I E H E T G T K I T I S S L Q D
Query:	1025	acaacccggaaagaaccatcactgtgaagggcacagttgaggcctgtgc
Sbjct:	1029	acaacccggaaagaaccatcactgtgaagggcacagttgaggcctgtgc
IGF-II mRNA-binding protein 2	318	Y N P E R T I T V K G T V E A C A
Query:	1085	tagagattatgaagaagctgcgtgaggcctttgaaaatgatatgctggc
Sbjct:	1089	tagagattatgaagaagctgcgtgaggcctttgaaaatgatatgctggc
IGF-II mRNA-binding protein 2	338	I E I M K K L R E A F E N D M L A
Query:	1145	aagccaatctgatcccaggggtgaacctcagcgcacttggcatcttttc
Sbjct:	1149	aagccaatctgatcccaggggtgaacctcagcgcacttggcatcttttc
IGF-II mRNA-binding protein 2	358	Q A N L I P G L N L S A L G I F S
Query:	1205	ccgtgctatctccaccagcagggcccccgcggagctcccccgctgcccc
Sbjct:	1209	ccgtgctatctccaccagcagggcccccgcggagctcccccgctgcccc
IGF-II mRNA-binding protein 2	378	S V L S P P A G P R G A P P A A P
Query:	1265	tcactaccactccggatacttctccagcctgtacccccatcaccagtt
Sbjct:	1269	tcactaccactccggatacttctccagcctgtacccccatcaccagtt
IGF-II mRNA-binding protein 2	398	F T T H S G Y F S S L Y P H H Q F
Query:	1325	cgcacatcactcttatccagagcaggagattgtgaatctcttcatccc
Sbjct:	1329	cgcacatcactcttatccagagcaggagattgtgaatctcttcatccc
IGF-II mRNA-binding protein 2	418	P H H H S Y P E Q E I V N L F I P
Query:	1385	tgggcgccatcatcggaagaagggggcacacatcaaacagctggcgag
Sbjct:	1389	tgggcgccatcatcggaagaagggggcacacatcaaacagctggcgag
IGF-II mRNA-binding protein 2	438	V G A I I G K K G A H I K Q L A R
Query:	1445	cctctatcaagattgccctgcggaaggcccagacgtcagcgaaaggat
Sbjct:	1449	cctctatcaagattgccctgcggaaggcccagacgtcagcgaaaggat
IGF-II mRNA-binding protein 2	458	A S I K I A P A E G P D V S E R M
Query:	1505	ccqqqccaccqqaagcccaqttcaagqcccaqqqacqqatctttqqqaa


```

Sbjct: 1509 cccgggccaccggaagcccagttcaaggcccaggacggatctttgggaa
IGF-II mRNA-binding protein 2 478 T G P P E A Q F K A Q G R I F G K

Query: 1565 aaaacttctttaaccccaaagaagaagtgaagctggaagcgcatatcag
Sbjct: 1569 aaaacttctttaaccccaaagaagaagtgaagctggaagcgcatatcag
IGF-II mRNA-binding protein 2 498 E N F F N P K E E V K L E A H I R

Query: 1625 ccacagctggccgggtgattggcaaaggtggcaagaccgtgaacgaact
Sbjct: 1629 ccacagctggccgggtgattggcaaaggtggcaagaccgtgaacgaact
IGF-II mRNA-binding protein 2 518 S T A G R V I G K G G K T V N E L

Query: 1685 ccagtgcagaagtcatcgctgcctcgtgaccaaacgccagatgaaaatga
Sbjct: 1689 ccagtgcagaagtcatcgctgcctcgtgaccaaacgccagatgaaaatga
IGF-II mRNA-binding protein 2 538 T S A E V I V P R D Q T P D E N E

Query: 1745 tcagaattatcgggcacttctttgctagccagactgcacagcgcaagat
Sbjct: 1749 tcagaattatcgggcacttctttgctagccagactgcacagcgcaagat
IGF-II mRNA-binding protein 2 558 V R I I G H F F A S Q T A Q R K I

Query: 1805 tacaacaggtgaagcagcaggagcagaaataccctcagggagtcgcctc
Sbjct: 1809 tacaacaggtgaagcagcaggagcagaaataccctcagggagtcgcctc
IGF-II mRNA-binding protein 2 578 V Q Q V K Q Q E Q K Y P Q G V A S

Query: 1865 agtgaggctccacaggcaccagcaaaacaacggatgaatgtagccctt
Sbjct: 1869 agtgaggctccacaggcaccagcaaaacaacggatgaatgtagccctt
IGF-II mRNA-binding protein 2 598 K ^^^

Query: 1925 cagaatgagaccaaacgcagccagccagatcgaggagcaaaccaagacc
Sbjct: 1929 cagaatgagaccaaacgcagccagccagatcgaggagcaaaccaagacc

Query: 1985 gagaagtctgcggaggcggccagggactctgccgaggccctgagaaccc
Sbjct: 1989 gagaagtctgcggaggcggccagggactctgccgaggccctgagaaccc

Query: 2045 gaggggcggggaaggtcagccaggtttgccagaaccaccgagccccgcc
Sbjct: 2049 gaggggcggggaaggtcagccaggtttgccagaaccaccgagccccgcc

Query: 2105 agggcttctgcaggcttcagccatccacttcaccatccactcggatctc
Sbjct: 2109 agggcttctgcaggcttcagccatccacttcaccatccactcggatctc

Query: 2165 cacgacgctatcccttttagttgaactaacataggtgaacgtgttcaaa
Sbjct: 2169 cacgacgctatcccttttagttgaactaacataggtgaacgtgttcaaa
```

Query: 2225 tgcacaccctttttctgtggcaaatacgtctctgtacatgtgtgtacata
|||||
Sbjct: 2229 tgcacaccctttttctgtggcaaatacgtctctgtacatgtgtgtacata

Query: 2285 agatgttaagatatgtggcctgtgggttacacagggcgctgcagcgg
|||||
Sbjct: 2289 agatgttaagatatgtggcctgtgggttacacagggcgctgcagcgg

Query: 2345 gaaataatatatcaaataactcaactaactccaatttttaataatcaattat
|||||
Sbjct: 2349 gaaataatatatcaaataactcaactaactccaatttttaataatcaattat

Query: 2405 nnnnnnnaagagaaagcaggcttttctagactttaagaataaagtct
|||||
Sbjct: 2409 tctttttaagagaaagcaggcttttctagactttaagaataaagtct

Query: 2465 cacgggtgtagagaggagctttgaggccacccgcacaaaattcacccaga
|||||
Sbjct: 2469 cacgggtgtagagaggagctttgaggccacccgcacaaaattcacccaga

Query: 2525 tcggaaggacactcacggcagttctggatcacctgtgtatgtcaacaga
|||||
Sbjct: 2529 tcggaaggacactcacggcagttctggatcacctgtgtatgtcaacaga

Query: 2585 ctccttgaagaggaaactctgtcactcctcatgcctgtctagctcatac
|||||
Sbjct: 2589 ctccttgaagaggaaactctgtcactcctcatgcctgtctagctcatac

Query: 2645 tttgcttcacaggttttaactgggtttttgcatactgctatataa 26
|||||
Sbjct: 2649 tttgcttcacaggttttaactgggtttttgcatactgctatataa 26

Score = 1040 bits (541), Expect = 0.0
Identities = 609/665 (91%), Gaps = 2/665 (0%)
Strand = Plus / Plus



Query: 2749 cattcttttgaatttcctcatccctccatctcaatcccgtatctacgcannnnnnnnnnn 2808
|||||
Sbjct: 2753 cattcttttgaatttcctcatccctccatctcaatcccgtatctacgcacccccccccc 2812

Query: 2809 nnaggcaaagcagtgtctgtgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 2868
|||||
Sbjct: 2813 c-aggcaaagcagtgtctgtgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 2871

Query: 2869 aaccagcctcaacttacacttggttactcaaaagaacaagagtcaatggtacttgccta 2928
|||||
Sbjct: 2872 aaccagcctcaacttacacttggttactcaaaagaacaagagtcaatggtacttgccta 2931

Query: 2929 gcgttttggagaggaaaacaggaacccaccaaaccaatcaaccaaacaagaaaa 2988
|||||
Sbjct: 2932 gcgttttggagaggaaaacaggaacccaccaaaccaatcaaccaaacaagaaaa 2991

```

Query: 2989 aattccacaatgaaagaatgtatTTTgtcTTTTgcattTTTggtgtataagccatcaata 3048
          |||
Sbjct: 2992 aattccacaatgaaagaatgtatTTTgtcTTTTgcattTTTggtgtataagccatcaata 3051

Query: 3049 ttcagcaaaatgattcctttcttt-nnnnnnnnnnnntgtggaggaaagtagaaatttacc 3107
          |||
Sbjct: 3052 ttcagcaaaatgattcctttctttaaaaaaaaaaaaatgtggaggaaagtagaaatttacc 3111

Query: 3108 aaggttggtggcccgaggcggttaaattcacagannnnnnnaacgagaaaaacacacagaa 3167
          |||
Sbjct: 3112 aaggttggtggcccgaggcggttaaattcacagattTTTtaacgagaaaaacacacagaa 3171

Query: 3168 gaagctacctcaggtgtTTTtacctcagcaccttgctcTTgtgtttcccttagagatttt 3227
          |||
Sbjct: 3172 gaagctacctcaggtgtTTTtacctcagcaccttgctcTTgtgtttcccttagagatttt 3231

Query: 3228 gtaaagctgatagttggagcannnnnnnnnnnnnnnaataaaaaatgagttggnnnnnnnnn 3287
          |||
Sbjct: 3232 gtaaagctgatagttggagcattTTTttattTTTtaataaaaaatgagttggaaaaaaa 3291

Query: 3288 taagatatcaactgccagcctggagaaggtgacagtcgaagtgcaacagctgttctga 3347
          |||
Sbjct: 3292 taagatatcaactgccagcctggagaaggtgacagtcgaagtgcaacagctgttctga 3351

Query: 3348 attgtcttccgctagccaagaacnataatggccttctTTTtgacaaaccttgaaaatggt 3407
          |||
Sbjct: 3352 attgtcttccgctagccaagaacctataatggccttctTTTtgacaaaccttgaaaatggt 3411

Query: 3408 tattt 3412
          |||
Sbjct: 3412 tattt 3416

```

CPU time: 0.06 user secs. 0.01 sys. secs 0.07 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
 Gap Penalties: Existence: 5, Extension: 2
 Number of Hits to DB: 13
 Number of Sequences: 0
 Number of extensions: 13
 Number of successful extensions: 8
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 0
 Number of HSP's gapped (non-prelim): 2
 length of query: 3412
 length of database: 8,918,056,233
 effective HSP length: 26

effective length of query: 3386
effective length of database: 8,918,056,207
effective search space: 30196538316902
effective search space used: 30196538316902
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 22 (43.0 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

●MIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

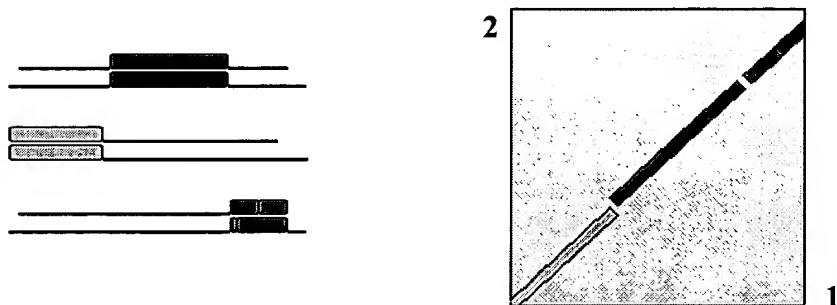
SE 8
27552765

Sequence 1 lcl|seq_1

Length 3283 (1 .. 3283)

Sequence 2 gi 27552765 Homo sapiens IGF-II mRNA-binding protein 2
(IMP-2), mRNA

Length 3642 (1 .. 3642)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 2675 bits (1391), Expect = 0.0
 Identities = 1406/1421 (98%)
 Strand = Plus / Plus

```
Query:                1141 acccactccggatacttctccagcctgtacccccatcaccagtttggcc
                        |||
Sbjct:                1274 acccactccggatacttctccagcctgtacccccatcaccagtttggcc
IGF-II mRNA-binding protein 2 400 T H S G Y F S S L Y P H H Q F G
```

```
Query:                1201 catcactcttatccagagcaggagattgtgaatctcttcatcccaaccc
                        |||
Sbjct:                1334 catcactcttatccagagcaggagattgtgaatctcttcatcccaaccc
IGF-II mRNA-binding protein 2 420 H H S Y P E Q E I V N L F I P T
```

```
Query:                1261 gccatcatcggaagaagggggcacacatcaaacagctggcgagattcg
                        |||
Sbjct:                1394 gccatcatcggaagaagggggcacacatcaaacagctggcgagattcg
IGF-II mRNA-binding protein 2 440 A I I G K K G A H I K Q L A R F
```

```
Query:                1321 atcaagattgccctgcggaaggcccagacgtcagcgaaaggatgggtca
                        |||
```

Sbjct:		1454	atcaagattgccctgcggaaggccagacgtcagtgaaaggatgggtca
IGF-II mRNA-binding protein 2	460		I K I A P A E G P D V S E R M V
Query:		1381	ccaccggaagcccagttcaaggcccaggacggatctttgggaaactga
Sbjct:		1514	ccaccggaagcccagttcaaggcccaggacggatctttgggaaactga
IGF-II mRNA-binding protein 2	480		P P E A Q F K A Q G R I F G K L
Query:		1441	ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgc
Sbjct:		1574	ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgc
IGF-II mRNA-binding protein 2	500		F F N P K E E V K L E A H I R V
Query:		1501	gctggccgggtgattggcaaagggtggcaagaccgtgaacgaactgcaga
Sbjct:		1634	gctggccgggtgattggcaaagggtggcaagaccgtgaacgaactgcaga
IGF-II mRNA-binding protein 2	520		A G R V I G K G G K T V N E L Q
Query:		1561	gcagaagtcatcgtgcctcgtgaccaaaccgacagatgaaaatgaggaag
Sbjct:		1694	gcagaagtcatcgtgcctcgtgaccaaaccgacagatgaaaatgaggaag
IGF-II mRNA-binding protein 2	540		A E V I V P R D Q T P D E N E E
Query:		1621	attatcgggcacttctttgctagccagactgcacagcgcaagatcaggg
Sbjct:		1754	attatcgggcacttctttgctagccagactgcacagcgcaagatcaggg
IGF-II mRNA-binding protein 2	560		I I G H F F A S Q T A Q R K I R
Query:		1681	cagggtgaagcagcaggagcagaaataccctcagggagtcgcctcacagc
Sbjct:		1814	cagggtgaagcagcaggagcagaaataccctcagggagtcgcctcacagc
IGF-II mRNA-binding protein 2	580		Q V K Q Q E Q K Y P Q G V A S Q
Query:		1741	ggctcccacaggcaccagcaaaacaacggatgaatgtagcccttccaac
Sbjct:		1874	ggctcccacaggcaccagcaaaacaacggatgaatgtagcccttccaac
Query:		1801	tgagaccaaaccgagccagccagatcgggagcaaaccaaagaccatctg
Sbjct:		1934	tgagaccaaaccgagccagccagatcgggagcaaaccaaagaccatctg
Query:		1861	gtctgcggaggcggccagggaactctgccgaggccctgagaacccaggg
Sbjct:		1994	gtctgcggaggcggccagggaactctgccgaggccctgagaacccaggg
Query:		1921	gcggggaaggtcagccaggtttgccagaaccaccgagccccgcctcccg
Sbjct:		2054	gcggggaaggtcagccaggtttgccagaaccaccgagccccgcctcccg
Query:		1981	ttctgcaggcttcagccatccacttcaccatccactcggatctctcctg
Sbjct:		2114	ttctgcaggcttcagccatccacttcaccatccactcggatctctcctg

```
Query:          2041 cgctatcccttttagttgaactaacataggtgaacgtgttcaaagccaa
                  |||
Sbjct:          2174 cgctatcccttttagttgaactaacataggtgaacgtgttcaaagccaa

Query:          2101 accctttttctgtggcaaactcgtctctgtacatgtgtgtacatattaga
                  |||
Sbjct:          2234 accctttttctgtggcaaactcgtctctgtacatgtgtgtacatattaga

Query:          2161 ttaagatatgtggcctgtgggttacacaggggtgcctgcagcggtaatat
                  |||
Sbjct:          2294 ttaagatatgtggcctgtgggttacacaggggtgcctgcagcggtaatat

Query:          2221 aatatatcaaataactcaactaactccaatttttaataattattaann
                  |||
Sbjct:          2354 aatatatcaaataactcaactaactccaatttttaataattattaatt

Query:          2281 nnaaagagaaagcaggcttttctagactttaagaataaagtctttggg
                  |||
Sbjct:          2414 ttaaagagaaagcaggcttttctagactttaagaataaagtctttggg

Query:          2341 tgtagagaggagctttgaggccaccgcacaaaattcacccagagggaa
                  |||
Sbjct:          2474 tgtagagaggagctttgaggccaccgcacaaaattcacccagagggaa

Query:          2401 aggacactcacggcagttctggatcacctgtgtatgtcaacagaagga
                  |||
Sbjct:          2534 aggacactcacggcagttctggatcacctgtgtatgtcaacagaagga

Query:          2461 tgaagaggaaactctgtcactcctcatgcctgtctagctcatacaccca
                  |||
Sbjct:          2594 tgaagaggaaactctgtcactcctcatgcctgtctagctcatacaccca

Query:          2521 ttcacaggttttaactgggtttttgcatactgctatataa 2561
                  |||
Sbjct:          2654 ttcacaggttttaactgggtttttgcatactgctatataa 2694
```

Score = 2184 bits (1136), Expect = 0.0

Identities = 1136/1136 (100%)

Strand = Plus / Plus



```
Query:          5   gcggaggaggcgaggagcgccgggtaccgggcccggggagccgcgggct
                  |||
Sbjct:          9   gcggaggaggcgaggagcgccgggtaccgggcccggggagccgcgggct

Query:          65   gacggatgatgaacaagctttacatcgggaacctgagccccgccgtcac
                  |||
Sbjct:          69   gacggatgatgaacaagctttacatcgggaacctgagccccgccgtcac
IGF-II mRNA-binding protein 2 1      M N K L Y I G N L S P A V T

Query:          125  tccggcagctctttggggacaggaagctgccctggcgggacaggtcct
                  |||
Sbjct:          129  tccggcagctctttggggacaggaagctgccctggcgggacaggtcct
```

IGF-II mRNA-binding protein 2 18 L R O L F G D R K L P L A G Q V L

```

Query:                185  gctacgccttcgtggactaccccgaccagaactgggccatccgcgccat
                        |||
Sbjct:                189  gctacgccttcgtggactaccccgaccagaactgggccatccgcgccat
IGF-II mRNA-binding  38  G Y A F V D Y P D Q N W A I R A I

```

```

Query:                245  cgggtaaagtggaattgcatgggaaaatcatggaagttgattactcagt
                        |||
Sbjct:                249  cgggtaaagtggaattgcatgggaaaatcatggaagttgattactcagt
IGF-II mRNA-binding  58  S G K V E L H G K I M E V D Y S V

```

```

Query:                305  taaggagcagggaaaattcagattcgaaacatccctcctcacctgcagtg
                        |||
Sbjct:                309  taaggagcagggaaaattcagattcgaaacatccctcctcacctgcagtg
IGF-II mRNA-binding protein 2 78  L R S R K I Q I R N I P P H L Q W

```

```
Query:                365 atggacttttggctcaatatgggacagtggagaatgtggaacaagtcaa
                        |||
Sbjct:                369 atggacttttggctcaatatgggacagtggagaatgtggaacaagtcaa
IGF-II mRNA-binding protein 2 98 D G L L A Q Y G T V E N V E Q V N
```

```

Query:                425 aaaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaat
                        |||
Sbjct:                429 aaaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaat
IGF-II mRNA-binding  118 E T A V V N V T Y A T R E E A K I

```

```

Query:                485  agctaagcgggcatcagtttgagaactactccttcaagatttcctacat
                        |||
Sbjct:                489  agctaagcgggcatcagtttgagaactactccttcaagatttcctacat
IGF-II mRNA-binding  138  K L S G H Q F E N Y S F K I S Y I

```

```

Query:                545  aggtgagctcccttcgccccctcagcgagcccagcgtggggaccactc
                        |||
Sbjct:                549  aggtgagctcccttcgccccctcagcgagcccagcgtggggaccactc
IGF-II mRNA-binding  158  E V S S P S P P Q R A Q R G D H S

```

```

Query:                605  aagggcacgcccctgggggcacttctcaggccagacagattgatttccc
                        |||
Sbjct:                609  aagggcacgcccctgggggcacttctcaggccagacagattgatttccc
IGF-II mRNA-binding  178  Q G H A P G G T S Q A R Q I D F P

```

```

Query:                665  ttggtccccacccagtttggttggtgccatcatcggaaggagggttgac
                        |||
Sbjct:                669  ttggtccccacccagtttggttggtgccatcatcggaaggagggttgac
IGF-II mRNA-binding  198  L V P T Q F V G A I I G K E G L T

```

```

Query:              725  tcactaagcagacccagtcctcggttagatatccatagaaaagagaactc
                        |||
Sbjct:              729  tcactaagcagacccagtcctcggttagatatccatagaaaagagaactc
IGF-II mRNA-binding protein 2 218  I T K Q T Q S R V D I H R K E N S

```

Query: 785 agaagcctgtcaccatccatgccacccagaggggacttctgaagcatg

Query: 2860 aattccacaatgaaagaatgtattttgtctttttgcattttggtgtataagccatcaata 2919
 |||
 Sbjct: 2992 aattccacaatgaaagaatgtattttgtctttttgcattttggtgtataagccatcaata 3051

Query: 2920 ttcagcaaaatgattcctttcttt-nnnnnnnnnntgtggaggaaagtagaaatttacc 2978
|||||
Sbjct: 3052 ttcagcaaaatgattcctttctttaaaaaaaaaaagtgaggaaagtagaaatttacc 3111

Query: 2979 aaggttggtggcccgaggcggttaaattcacagannnnnnnaacgagaaaaacacacagaa 3038
|||||
Sbjct: 3112 aaggttggtggcccgaggcggttaaattcacagatttttttaacgagaaaaacacacagaa 3171

Query: 3039 gaagctacctcaggtgtttttacctcagcaccttgctcttggtttcccttagagatttt 3098
|||||
Sbjct: 3172 gaagctacctcaggtgtttttacctcagcaccttgctcttggtttcccttagagatttt 3231

Query: 3099 gtaaagctgatagttggagcannnnnnnnnnnnnaataaaaaatgagttggnnnnnnnn 3158
|||||
Sbjct: 3232 gtaaagctgatagttggagcattttttttatttttttaataaaaaatgagttggaaaaaaa 3291

Query: 3159 taagatatcaactgccagcctggagaaggtgacagtccaagtgtgcaacagctgttctga 3218
|||||
Sbjct: 3292 taagatatcaactgccagcctggagaaggtgacagtccaagtgtgcaacagctgttctga 3351

Query: 3219 attgtcttccgctagccaagaacnataatggccttcttttgacaaaccttgaaaatggt 3278
|||||
Sbjct: 3352 attgtcttccgctagccaagaacctatatggccttcttttgacaaaccttgaaaatggt 3411

Query: 3279 tatttt 3283
|||||
Sbjct: 3412 tatttt 3416

CPU time: 0.04 user secs. 0.00 sys. secs 0.04 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 14
Number of Sequences: 0
Number of extensions: 14
Number of successful extensions: 9
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 5
length of query: 3283
length of database: 8,918,056,233
effective HSP length: 26
effective length of query: 3257
effective length of database: 8,918,056,207
effective search space: 29046109066199
effective search space used: 29046109066199
T: 0
A: 0
X1: 6 (11.5 bits)

X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 22 (43.0 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

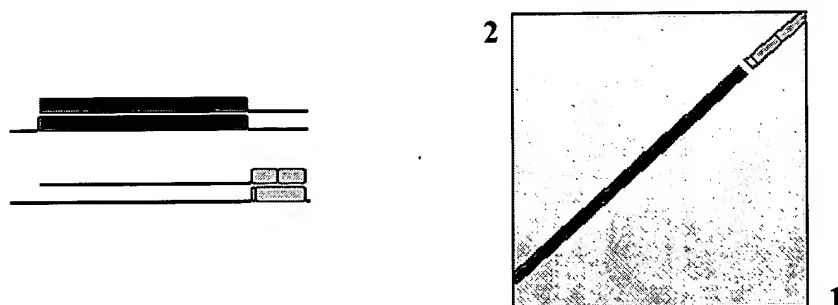
Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

SEQ 8
gi 4883680

Sequence 1 lcl|seq_1 Length 3283 (1 .. 3283)

Sequence 2 gi 4883680 Length 3667 (1 .. 3667)

(hepatocellular)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 4857 bits (2526), Expect = 0.0
 Identities = 2541/2556 (99%)
 Strand = Plus / Plus



```

Query:          6  cggaggaggcgaggagcgccgggtaccgggccccggggagccgcggg
                  |||
Sbjct:         372  cggaggaggcgaggagcgccgggtaccgggccccggggagccgcggg

Query:          66  acggatgatgaacaagctttacatcgggaaacctgagccccgccgtc
                  |||
Sbjct:         432  acggatgatgaacaagctttacatcgggaaacctgagccccgccgtc
hepatocellular carcinoma autoan> 1      M M N K L Y I G N L S P A V

Query:          126  ccggcagctctttggggacaggaagctgcccctggcgggacaggtc
                  |||
Sbjct:         492  ccggcagctctttggggacaggaagctgcccctggcgggacaggtc
hepatocellular carcinoma autoan> 20      R Q L F G D R K L P L A G Q V

Query:          186  ctacgccttcgtggactaccccgaccagaactgggccatccgcgcc
                  |||
Sbjct:         552  ctacgccttcgtggactaccccgaccagaactgggccatccgcgcc
hepatocellular carcinoma autoan> 40      Y A F V D Y P D Q N W A I R A
  
```

```
Query: 246 gggtaaagtgggaattgcatgggaaaatcatggaagttgattactca
      |||
Sbjct: 612 gggtaaagtgggaattgcatgggaaaatcatggaagttgattactca
hepatocellular carcinoma autoan> 60 G K V E L H G K I M E V D Y S

Query: 306 aaggagcaggaaaattcagattcgaaacatccctcctcacctgcag
      |||
Sbjct: 672 aaggagcaggaaaattcagattcgaaacatccctcctcacctgcag
hepatocellular carcinoma autoan> 80 R S R K I Q I R N I P P H L Q

Query: 366 tggacttttggctcaatatgggacagtggagaatgtggaacaagtc
      |||
Sbjct: 732 tggacttttggctcaatatgggacagtggagaatgtggaacaagtc
hepatocellular carcinoma autoan> 100 G L L A Q Y G T V E N V E Q V

Query: 426 aaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaa
      |||
Sbjct: 792 aaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaa
hepatocellular carcinoma autoan> 120 T A V V N V T Y A T R E E A K

Query: 486 gctaagcgggcatcagtttgagaactactccttcaagatttcctac
      |||
Sbjct: 852 gctaagcgggcatcagtttgagaactactccttcaagatttcctac
hepatocellular carcinoma autoan> 140 L S G H Q F E N Y S F K I S Y

Query: 546 ggtgagctcccccttcgccccctcagcgagcccagcgtggggaccac
      |||
Sbjct: 912 ggtgagctcccccttcgccccctcagcgagcccagcgtggggaccac
hepatocellular carcinoma autoan> 160 V S S P S P P Q R A Q R G D H

Query: 606 aggccacgcccctgggggcacttctcaggccagacagattgatttc
      |||
Sbjct: 972 aggccacgcccctgggggcacttctcaggccagacagattgatttc
hepatocellular carcinoma autoan> 180 G H A P G G T S Q A R Q I D F

Query: 666 ggtccccacccagtttggttggtgccatcatcggaaggagggttg
      |||
Sbjct: 1032 ggtccccacccagtttggttggtgccatcatcggaaggagggttg
hepatocellular carcinoma autoan> 200 V P T Q F V G A I I G K E G L

Query: 726 cactaagcagaccagtcgccgggtagatatccatagaaaagagaaac
      |||
Sbjct: 1092 cactaagcagaccagtcgccgggtagatatccatagaaaagagaaac
hepatocellular carcinoma autoan> 220 T K Q T Q S R V D I H R K E N

Query: 786 gaagcctgtcaccatccatgccaccccagaggggacttctgaagca
      |||
Sbjct: 1152 gaagcctgtcaccatccatgccaccccagaggggacttctgaagca
hepatocellular carcinoma autoan> 240 K P V T I H A T P E G T S E A

Query: 846 tgaaatcatgcagaaagaggcagatgagaccaaactagccgaagag
      |||
Sbjct: 1212 tgaaatcatgcagaaagaggcagatgagaccaaactagccgaagag
hepatocellular carcinoma autoan> 260 E I M Q K E A D E T K L A E E
```

```

Query:                               906  cttggcacacaatggcttggttgaagactgattggaaaagaaggc
      ||||||||||||||||||||||||||||||||||||||||||||
Sbjct:                               1272  cttggcacacaatggcttggttgaagactgattggaaaagaaggc
hepatocellular carcinoma autoan> 280   L A H N G L V G R L I G K E G

```

```

Query:                                     966 aattgaacatgaaacagggaccaagataacaatctcatctttgcag
      ||||||||||||||||||||||||||||||||||||||||||||
Sbjct:                                     1332 aattgaacatgaaacagggaccaagataacaatctcatctttgcag
hepatocellular carcinoma autoan> 300   I E H E T G T K I T I S S L Q

```

```

Query:                                     1026 caaccggaaagaaccatcactgtgaagggcacagttgaggcctgt
      |||||||||||||||||||||||||||||||||||||||||
Sbjct:                                     1392 caaccggaaagaaccatcactgtgaagggcacagttgaggcctgt
hepatocellular carcinoma autoan> 320      N P E R T I T V K G T V E A C

```

```

Query:                                     1086 agagattatgaagaagctgcgtgaggcctttgaaaatgatatgctg
      |||||||||||||||||||||||||||||||||||||||||||
Sbjct:                                     1452 agagattatgaagaagctgcgtgaggcctttgaaaatgatatgctg
hepatocellular carcinoma autoan> 340      E I M K K L R E A F E N D M L

```

```

Query:                               1146 ctccggatacttctccagcctgtacccccatcaccagtttgcccg
      |||||||||||||||||||||||||||||||||||||||
Sbjct:                               1512 ctccggatacttctccagcctgtacccccatcaccagtttgcccg
hepatocellular carcinoma autoan> 360   S G Y F S S L Y P H H Q F G P

```

```

Query:                               1206 ctcttatccagagcaggagattgtgaatctcttcatcccaaccag
      |||||||||||||||||||||||||||||||||||||||
Sbjct:                               1572 ctcttatccagagcaggagattgtgaatctcttcatcccaaccag
hepatocellular carcinoma autoan> 380   S Y P E Q E I V N L F I P T Q

```

```

Query:                               1266 catcgggaagaaggggggcacacatcaaacagctggcgagattcgcc
                                   |||
Sbjct:                               1632 catcgggaagaaggggggcacacatcaaacagctggcgagattcgcc
hepatocellular carcinoma autoan> 400  I G K K G A H I K Q L A R F A

```

```
Query: 1326 gattgccctgcggaaggcccagacgtcagcgaaaggatgggtcatc
      ||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1692 gattgccctgcggaaggcccagacgtcagcgaaaggatgggtcatc
hepatocellular carcinoma autoan> 420 I A P A E G P D V S E R M V I
```

```
Query: 1386 ggaagcccagttcaaggcccgaggacggatctttgggaaactgaaa
      |||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1752 ggaagcccagttcaaggcccgaggacggatctttgggaaactgaaa
hepatocellular carcinoma autoan> 440 E A Q F K A Q G R I F G K L K
```

```

Query:      1446 taaccccaaagaagaagtgaagctggaagcgcatatcagagtgcc
             |||
Sbjct:      1812 taaccccaaagaagaagtgaagctggaagcgcatatcagagtgcc
hepatocellular carcinoma autoan> 460   N P K E E V K L E A H I R V P

```

Query: 1506 ccgggtgattggcaaaggtggcaagaccgtgaacgaactgcagaac
| | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 1872 ccgggtgat tggcaaaggtggcaagaccgtgaacgaactgcagaac

```
hepatocellular carcinoma autoan> 480      R V I G K G G K T V N E L Q N

Query:          1566 agtcatcgtgcctcgtgaccaaacgccagatgaaaatgaggaagtg
                  |||
Sbjct:          1932 agtcatcgtgcctcgtgaccaaacgccagatgaaaatgaggaagtg
hepatocellular carcinoma autoan> 500      V I V P R D Q T P D E N E E V

Query:          1626 cgggcacttctttgctagccagactgcacagcgcaagatcagggaa
                  |||
Sbjct:          1992 cgggcacttctttgctagccagactgcacagcgcaagatcagggaa
hepatocellular carcinoma autoan> 520      G H F F A S Q T A Q R K I R E

Query:          1686 gaagcagcaggagcagaaataccctcagggagtcgcctcacagcgc
                  |||
Sbjct:          2052 gaagcagcaggagcagaaataccctcagggagtcgcctcacagcgc
hepatocellular carcinoma autoan> 540      K Q Q E Q K Y P Q G V A S Q R

Query:          1746 ccacaggcaccagcaaaacaacggatgaatgtagcccttccaacac
                  |||
Sbjct:          2112 ccacaggcaccagcaaaacaacggatgaatgtagcccttccaacac

Query:          1806 ccaaacgcagccagccagatcgggagcaaaccaaagaccatctgag
                  |||
Sbjct:          2172 ccaaacgcagccagccagatcgggagcaaaccaaagaccatctgag

Query:          1866 cggaggcgggccagggactctgccgaggccctgagaaccccgagggg
                  |||
Sbjct:          2232 cggaggcgggccagggactctgccgaggccctgagaaccccgagggg

Query:          1926 gaaggtcagccaggtttgccagaaccaccgagccccgcctcccgcc
                  |||
Sbjct:          2292 gaaggtcagccaggtttgccagaaccaccgagccccgcctcccgcc

Query:          1986 caggcttcagccatccacttcaccatccactcggatctctcctgaa
                  |||
Sbjct:          2352 caggcttcagccatccacttcaccatccactcggatctctcctgaa

Query:          2046 tcccttttagttgaactaacataggtgaacgtgttcaaagccaagc
                  |||
Sbjct:          2412 tcccttttagttgaactaacataggtgaacgtgttcaaagccaagc

Query:          2106 ttttctgtggcaaatacgtctctgtacatgtgtgtacatattagaaa
                  |||
Sbjct:          2472 ttttctgtggcaaatacgtctctgtacatgtgtgtacatattagaaa

Query:          2166 atatgtggcctgtgggttacacaggggtgcctgcagcggtaatatat
                  |||
Sbjct:          2532 atatgtggcctgtgggttacacaggggtgcctgcagcggtaatatat

Query:          2226 atcaaataactcaactaactccaatttttaataattattaannnn
                  |||
Sbjct:          2592 atcaaataactcaactaactccaatttttaataattattaatttt
```

Query: 2286 gagaaagcaggcttttctagactttaagaataaagtctttgggag
|||||
Sbjct: 2652 gagaaagcaggcttttctagactttaagaataaagtctttgggag

Query: 2346 agaggagctttgaggccacccgcacaaaattcacccagagggaaat
|||||
Sbjct: 2712 agaggagctttgaggccacccgcacaaaattcacccagagggaaat

Query: 2406 actcacggcagttctggatcacctgtgtatgtcaacagaagggata
|||||
Sbjct: 2772 actcacggcagttctggatcacctgtgtatgtcaacagaagggata

Query: 2466 aggaaactctgtcactcctcatgcctgtctagctcatacaccatt
|||||
Sbjct: 2832 aggaaactctgtcactcctcatgcctgtctagctcatacaccatt

Query: 2526 aggttttaactggttttttgcatactgctatataa 2561
|||||
Sbjct: 2892 aggttttaactggttttttgcatactgctatataa 2927

Score = 1035 bits (538), Expect = 0.0
Identities = 608/665 (91%), Gaps = 2/665 (0%)
Strand = Plus / Plus

Query: 2620 cattcttttgaatttcctcatccctccatctcaatcccgtatctacgcannnnnnnnnnn 2679
|||||
Sbjct: 2986 cattcttttgaatttcctcatccctccatctcaatcccgtatctacgcacccccccccc 3045

Query: 2680 nnaggcaaagcagtgtctgtgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 2739
|||||
Sbjct: 3046 c-aggcaaagcagtgtctgtgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 3104

Query: 2740 aaccagcctcaacttacacttgggttactcaaaagaacaagagtcaatgggtacttgtccta 2799
|||||
Sbjct: 3105 aaccagcctcaacttacacttgggttactcaaaagaacaagagtcaatgggtacttgtccta 3164

Query: 2800 gcgttttgggaagaggaaaacaggaacccaccaaaccaacaaatcaaccaaacaagaaaa 2859
|||||
Sbjct: 3165 gcgttttgggaagaggaaaacaggaacccaccaaaccaacaaatcaaccaaacaagaaaa 3224

Query: 2860 aattccacaatgaaagaatgtattttgcattttgggtgtataagccatcaata 2919
|||||
Sbjct: 3225 aattccacaatgaaagaatgtattttgcattttgggtgtataagccatcaata 3284

Query: 2920 ttcagcaaatgattcctttcttt-nnnnnnnnnntgtggaggaaagtagaaatttacc 2978
|||||
Sbjct: 3285 ttcagcaaatgattcctttctttaaaaaaaaaaagtgaggaggaaagtagaaatttacc 3344

Query: 2979 aaggttggtggccaggcggttaaattcacagannnnnnnaacgagaaaaacacacagaa 3038
|||||
Sbjct: 3345 aaggttggtggccaggcggttaaattcacagatttttttaacgagaaaaacacacagaa 3404

Query: 3039 gaagctacctcaggtgtttttacctcagcaccttgctcttggtgtttcccttagagatttt 3098
|||||
Sbjct: 3405 gaagctacctcaggtgtttttacctcagcaccttgatcttggtgtttcccttagagatttt 3464

Query: 3099 gtaaagctgatagttggagcannnnnnnnnnnnnaataaaaaatgagttggnnnnnnnn 3158
|||||
Sbjct: 3465 gtaaagctgatagttggagcatttttttatttttttaataaaaaatgagttggaaaaaaaa 3524

Query: 3159 taagatatcaactgccagcctggagaaggtgacagtccaagtgtgcaacagctgttctga 3218
|||||
Sbjct: 3525 taagatatcaactgccagcctggagaaggtgacagtccaagtgtgcaacagctgttctga 3584

Query: 3219 attgtcttccgctagccaagaacnatatggccttcttttggacaaaccttgaaaatgtt 3278
|||||
Sbjct: 3585 attgtcttccgctagccaagaacctatatggccttcttttggacaaaccttgaaaatgtt 3644

Query: 3279 tattt 3283
|||||
Sbjct: 3645 tattt 3649

CPU time: 0.05 user secs. 0.00 sys. secs 0.05 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 13
Number of Sequences: 0
Number of extensions: 13
Number of successful extensions: 8
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 2
length of query: 3283
length of database: 8,918,056,233
effective HSP length: 26
effective length of query: 3257
effective length of database: 8,918,056,207
effective search space: 29046109066199
effective search space used: 29046109066199
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 22 (43.0 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

c-myc-CRD

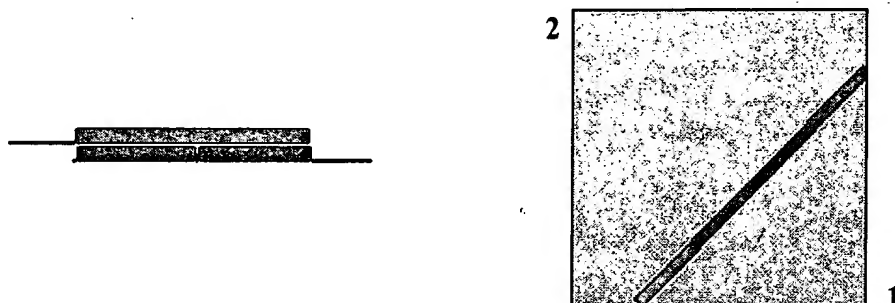
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:5

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** ☐ Filter ☐ Align

Sequence 1 lcl|seq_1 Length 577 (1 .. 577)

Sequence 2 lcl|seq_2 Length 1708 (1 .. 1708)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 854 bits (2206), Expect = 0.0
Identities = 438/445 (98%), Positives = 439/445 (98%)
Frame = +2

```
Query: 133 RQAIMKLNQHLENHALKVSYPDEQITQGPENGRGGFGSRGQPRQGSPPVAAGAPAKQQ 192
          R AIMKLNQHLENHALKVSYPDEQI QGPENGRGGFGSRGQPRQGSPPVAAGAPAKQQ
Sbjct: 32  RGAIMKLNQHLENHALKVSYPDEQIAQGPENGRGGFGSRGQPRQGSPPVAAGAPAKQQ 211

Query: 193 PVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 252
          VDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG
Sbjct: 212 QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 391

Query: 253 CSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLLIGKEGRNLKKVEQDTETKITI 312
          CSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLLIGKEGRNLKKVEQDTETKITI
Sbjct: 392 CSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLLIGKEGRNLKKVEQDTETKITI 571

Query: 313 SSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMSLQSHLIPGLNLAA 372
          SSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS SHLIPGLNLAA
Sbjct: 572 SSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS --SHLIPGLNLAA 745

Query: 373 VGLFPASSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLS 432
          VGLFPASSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLS
Sbjct: 746 VGLFPASSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLS 925

Query: 433 RFASASIKIAPPETPDSKVRMVITGPPEAQFKAQGRIYGKLKEENFFGPKEEVKLETHI 492
          RFASASIKIAPPETPDSKVRMV+ITGPPEAQFKAQGRIYGKLKEENFFGPKEEVKLETHI
Sbjct: 926 RFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEENFFGPKEEVKLETHI 1105

Query: 493 RVPASAAGRVIGGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRK 552
          RVPASAAGRVIGGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRK
```

Sbjct: 1106RVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRK 1285

Query: 553 IRDILAQVKQQHQKGQSNLAQARRK 577

IRDILAQVKQQHQKGQSN AQARRK

Sbjct: 1286IRDILAQVKQQHQKGQSNQAQARRK 1360

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 11,732

Number of Sequences: 0

Number of extensions: 7631

Number of successful extensions: 15

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 2

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

c-myc-CRD

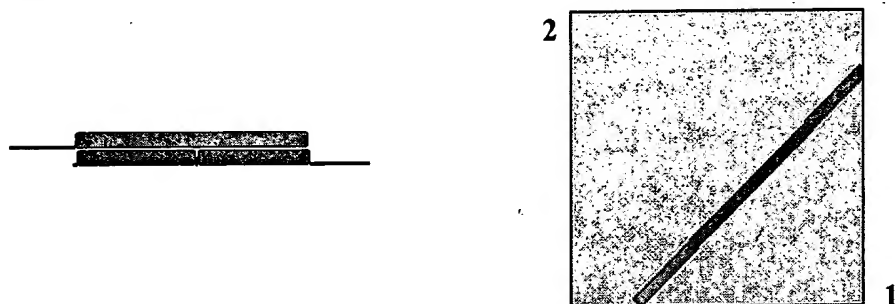
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:5

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0** wordsize: **3** ☐ Filter ☐ Align

Sequence 1 lcl|seq_1 Length 577 (1 .. 577)

Sequence 2 lcl|seq_2 Length 1708 (1 .. 1708)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 854 bits (2206), Expect = 0.0
 Identities = 438/445 (98%), Positives = 439/445 (98%)
 Frame = +2

```

Query: 133 RQAIMKLNQHLENHALKVSYPDEQITQGPENGRGGFGSRGQPRQGSPPVAAGAPAKQQ 192
          R AIMKLNQHLENHALKVSYPDEQI QGPENGRGGFGSRGQPRQGSPPVAAGAPAKQQ
Sbjct: 32  RQAIMKLNQHLENHALKVSYPDEQIAQGPENGRGGFGSRGQPRQGSPPVAAGAPAKQQ 211

Query: 193 PVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 252
          VDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG
Sbjct: 212 QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 391

Query: 253 CSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLLIGKEGRNLKKVEQDTETKITI 312
          CSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLLIGKEGRNLKKVEQDTETKITI
Sbjct: 392 CSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLLIGKEGRNLKKVEQDTETKITI 571

Query: 313 SSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMSLQSHLIPGLNLAA 372
          SSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS SHLIPGLNLAA
Sbjct: 572 SSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS--SHLIPGLNLAA 745

Query: 373 VGLFPASSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLS 432
          VGLFPASSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLS
Sbjct: 746 VGLFPASSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLS 925

Query: 433 RFASASIKIAPPETPDSKVRMVITGPPEAQFKAQGRIYGLKKEENFFGPKKEEVKLETHI 492
          RFASASIKIAPPETPDSKVRMV+ITGPPEAQFKAQGRIYGLKKEENFFGPKKEEVKLETHI
Sbjct: 926 RFASASIKIAPPETPDSKVRMVITGPPEAQFKAQGRIYGLKKEENFFGPKKEEVKLETHI 1105

Query: 493 RVPASAAGRVIGGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIIGHFYASQMAQRK 552
          RVPASAAGRVIGGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIIGHFYASQMAQRK
  
```

Sbjct: 1106RVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIIGHFYASQMAQRK 1285

Query: 553 IRDILAQVKQQHQKGQSNLAQARRK 577

IRDILAQVKQQHQKGQSN AQARRK

Sbjct: 1286IRDILAQVKQQHQKGQSNQAQARRK 1360

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 11,732

Number of Sequences: 0

Number of extensions: 7631

Number of successful extensions: 15

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 2

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

●MIM

Taxonomy

Structure

c-myc-CRD

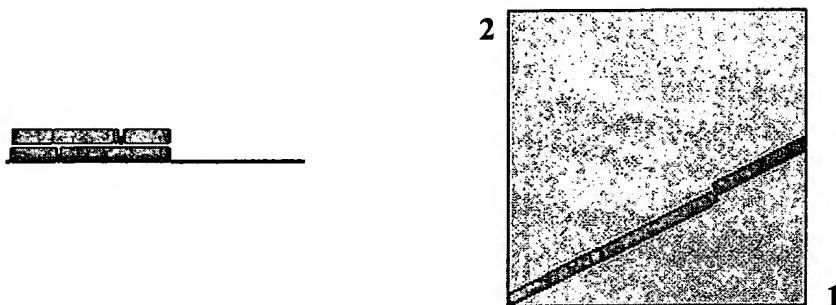
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:6

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align ☐

Sequence 1 lcl|seq_1 Length 577 (1..577)

Sequence 2 lcl|seq_2 Length 3412 (1..3412)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 775 bits (2000), Expect = 0.0
 Identities = 394/603 (65%), Positives = 476/603 (78%), Gaps = 26/603 (4%)
 Frame = +1

```

Query: 1  MNKLYIGNLNESVTPADLEKVFAEHKISYSGQFLVKSGYAFVDCPDEHWAMKAIETFSGK 60
          MNKLYIGNL+ +VT DL ++F + K+ +GQ L+KSGYAFVD PD++WA++AIET SGK
Sbjct: 73  MNKLYIGNLSPAVTADDLRQLFGDRKLPLAGQVLLKSGYAFVDYPDQNWAIETLSGK 252

Query: 61  VELQGRLEMEHSVPKKQSRKIQIRNIPPQLRWEVLDSLLAQYGTVENCEQVNTSEETA 120
          VEL GK +E+++SV KK RSRKIQIRNIPP L+WEVLD LLAQYGTVEN EQVNT++ETA
Sbjct: 253  VELHGKIMEVDYSVSKKLRSRKIQIRNIPPHLQWEVLDDGLLAQYGTVENVEQVNTDTETA 432

Query: 121  VVNVTYSNREQTRQAIMKLNQHLENHALKVSYPDEQITQG--PENGRRGGFGSRGQPR 178
          VVNVTY+ RE+ + A+ KL+GHQ EN++ K+SYIPDE+++ P+ +RG SR Q
Sbjct: 433  VVNVTYATREEAKIAMKLSGHQFENYSFKISYIPDEEVSSPSPPPQRAQRGDHSSREQGH 612

Query: 179  QGSPVAAGAPAKQQPVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAG 238
          A G ++ + +D PLR+LVPTQ+VGAIIGKEG TI+NITKQTQS++D+HRKEN+G
Sbjct: 613  -----APGGTSQARQIDFPLRILVPTQFVGAIIGKEGLTIKNITKQTQSRVDIHRKENSG 777

Query: 239  AAEKAISVHSTPEGCSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRILIGKEGRN 298
          AAEK +++H+TPEG S AC+MILEIM KEA +TK A+E+PLKILAHN VGRILIGKEGRN
Sbjct: 778  AAEKPVTIHATPEGTSEACRMILEIMQKEADETKLAEIPLKILAHNGLVGRILIGKEGRN 957

Query: 299  LKKVEQDTETKITISSLQDLTLNPERTITVKGAIEGCCRAEQEIMKKVREAYENDVAAM 358
          LKK+E +T TKITISSLQDL++YNPERTITVKG +E C AE EIMKK+REA+END+ A+
Sbjct: 958  LKKIEHETGTKITISSLQDLNPERTITVKGTVACASAEIEMKKLREAFENDMLAV 1137

Query: 359  SLQSHLIPGLNLAAVGLFPASSSAVPPP--PSSVTGAAPYSSFM----- 400
          + Q++LIPGLNL+A+G+F S + PP P AAPY F
  
```

Sbjct: 1138NQQANLIPGLNLSALGIFSTGLSVLSPPAGPRGAPPAAPYHPFTTHSGYFSSLYPHHQFG 1317

Query: 401 -----QAPEQEMVQVFIPAQAVGAIIGKKGQHILQLSRFASASIKIAPPETPDSKVRMV 454
PEQE+V +FIP QAVGAIIGKKG HIKQL+RFA ASIKIAP E PD . RMV

Sbjct: 1318PPPHHSYPEQEIVNLFIPTQAVGAIIGKKGAHIKQLARFAGASIKIAPAEGPDVSEMV 1497

Query: 455 VITGPPEAQFKAQGRIYGLKEENFFGPKEEVKLETHIRVPASAAGRVIGKGGKTVNELQ 514
+ITGPPEAQFKAQGRI+GKLKEENFF PKEEVKLE HIRVP+S AGRVIGKGGKTVNELQ

Sbjct: 1498IITGPPEAQFKAQGRIFGKLKEENFFNPKEEVKLEAHIRVPSSTAGRVIGKGGKTVNELQ 1677

Query: 515 NLTAEEVVPRDQTPDENQVIVKIIGHFYASQMAQRKIRDILAQVKQHQKQSNLAQA 574
NLT+AEV+VPRDQTPDEN++VIV+IIGHF+ASQ AQRKIR+I+ QVKQQ QK +A

Sbjct: 1678NLTSAEVIVPRDQTPDENEEVIVRIIGHFFASQTAQRKIREIVQVKQEQKYPQGVASQ 1857

Query: 575 RRK 577

R K

Sbjct: 1858RSK 1866

CPU time: 0.07 user secs. 0.00 sys. secs 0.07 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 21,798

Number of Sequences: 0

Number of extensions: 14808

Number of successful extensions: 17

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 3

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 3

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

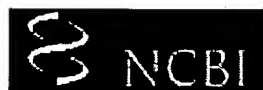
X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

c-myc-CRD

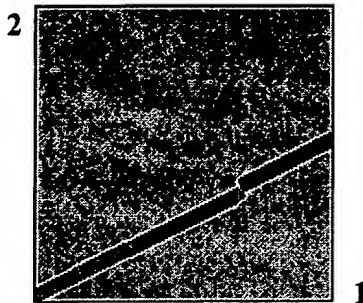
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:6

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align ☐

Sequence 1 lcl|seq_1 Length 577 (1..577)

Sequence 2 lcl|seq_2 Length 3412 (1..3412)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 775 bits (2000), Expect = 0.0
Identities = 394/603 (65%), Positives = 476/603 (78%), Gaps = 26/603 (4%)
Frame = +1

Query: 1 MNKLYIGNLNESVTPADLEKVFAEHKISYSGQFLVKSGYAFVDCPDEHWAMKAIETFS GK 60
MNKLYIGNL+ +VT DL ++F + K+ +GQ L+KSGYAFVD PD++WA++AIET SGK
Sbjct: 73 MNKLYIGNLSPAVTADDLRQLFGDRKLPLAGQVLLKSGYAFVDYPDQNWAIETLSGK 252

Query: 61 VELQGKRLEMEHSVPKKQRSRKIQIRNIPPQLRWEVLDSLLAQYGTVENCEQVNTSEETA 120
VEL GK +E+++SV KK RSRKIQIRNIPP L+WEVLD LLAQYGTVEN EQVNT++ETA
Sbjct: 253 VELHGKIMEVDYSVSKLRSRKIQIRNIPPHLQWEVLDGLLAQYGTVENVEQVNTDTETA 432

Query: 121 VVNVITYSNREQTRQAIMKLNQHLENHALKVSYPDEQITQG--PENGRRGGFGSRGQPR 178
VVNVTY+ RE+ + A+ KL+GHQ EN++ K+SYIPDE+++ P+ +RG SR Q
Sbjct: 433 VVNVTYATREEAKIAMEKLSGHQFENYSFKISYIPDEEVSSPSPQRAQRGDHSSREQGH 612

Query: 179 QGSPVAAGAPAKQQPVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQS KIDVHRKENAG 238
A G ++ + +D PLR+LVPTQ+VGAIIGKEG TI+NITKQTQS++D+HRKEN+G
Sbjct: 613 -----APGGTSQARQIDFPLRILVPTQFVGAIIGKEGLTIKNTKQTQSRVDIHRKENS G 777

Query: 239 AAEKAISVHSTPEGCSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGR LIGKEGRN 298
AAEK +++H+TPEG S AC+MILEIM KEA +TK A+E+PLKILAHN VGR LIGKEGRN
Sbjct: 778 AAEKPVTIHATPEGTSEACRMILEIMQKEADETKLAEIPLKILAHNGLVGR LIGKEGRN 957

Query: 299 LKKVEQDTEKITISSLQDLTLNPERTITVKGA IENCCRAEQEIMKKVREAYENDVAAM 358
LKK+E +T TKITISSLQDL++YNPERTITVKG +E C AE EIMKK+REA+END+ A+
Sbjct: 958 LKKIEHETGKITISSLQDL SIYNPERTITVKGTVEACASAEIEMKKLREAFENDMLAV 1137

Query: 359 SLQSHLIPGLNLAAVGLFPASSAVPPP--PSSVTGAAPYSSFM----- 400
+ Q++LIPGLNL+A+G+F S + PP P AAPY F

Sbjct: 1138NQQANLIPGLNLSALGIFSTGLSVLSPPAGPRGAPPAAPYHPFTTHSGYFSSLYPHHQFG 1317

Query: 401 -----QAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMV 454
PEQE+V +FIP QAVGAIIGKKG HIKQL+RFA ASIKIAP E PD RMV

Sbjct: 1318PFPHHHSYPEQEIVNLFIPTQAVGAIIGKKGAHIKQLARFAGASIKIAPAEGPDVSERMV 1497

Query: 455 VITGPPEAQFKAQGRIYGLKEENFFGPKKEEVKLETHIRVPASAAGRVIKGGKTVNELQ 514
+ITGPPEAQFKAQGRI+GKLKEENFF PKEEVKLE HIRVP+S AGRVIKGGKTVNELQ

Sbjct: 1498IITGPPEAQFKAQGRIFGKLKEENFFNPKEEVKLEAHIRVPSSTAGRVIGKGGKTVNELQ 1677

Query: 515 NLTAAEVVPRDQTPDENQVIVKIIGHFYASQMAQRKIRDILAQVKQHQKQSNLAQA 574
NLT+AEV+VPRDQTPDEN++VIV+IIGHF+ASQ AQRKIR+I+ QVKQQ QK +A

Sbjct: 1678NLTSAEVIVPRDQTPDENEEVIVRIIGHFFASQTAQRKIREIVQVKQEQKYPQGVASQ 1857

Query: 575 RRK 577

R K

Sbjct: 1858RSK 1866

CPU time: 0.07 user secs. 0.00 sys. secs 0.07 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 21,798

Number of Sequences: 0

Number of extensions: 14808

Number of successful extensions: 17

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 3

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 3

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

c-myc-CRD

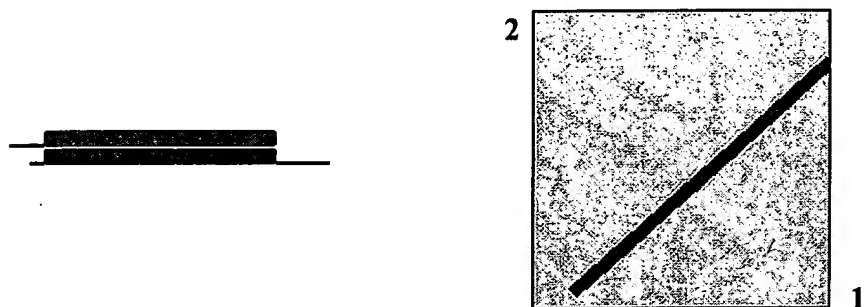
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:7

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align

Sequence 1 lcl|seq_1 Length 577 (1..577)

Sequence 2 lcl|seq_2 Length 1946 (1..1946)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 963 bits (2489), Expect = 0.0
Identities = 493/499 (98%), Positives = 494/499 (98%)
Frame = +3

Query: 79 RSRKIQIRNIPPQLRWEVLDSLLAQYGTVENCEQVNTSESETAVVNVITYSNREQTRQAIMK 138
RSRKIQIRNIPPQLRWEVLDSLLAQYGTVENCEQVNTSESETAVVNVITYSNREQTRQAIMK
Sbjct: 108 RSRKIQIRNIPPQLRWEVLDSLLAQYGTVENCEQVNTSESETAVVNVITYSNREQTRQAIMK 287

Query: 139 LNGHQLENHALKVSYPDEQITQGPENRRGGFGSRGQPRQGSPVAAGAPAKQQPVDIPL 198
LNGHQLENHALKVSYPDEQI QGPENRRGGFGSRGQPRQGSPVAAGAPAKQQ VDIPL
Sbjct: 288 LNGHQLENHALKVSYPDEQIAQGPENRRGGFGSRGQPRQGSPVAAGAPAKQQQVDIPL 467

Query: 199 RLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEGCSSACK 258
RLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEGCSSACK
Sbjct: 468 RLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEGCSSACK 647

Query: 259 MILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITISSLQDL 318
MILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITISSLQDL
Sbjct: 648 MILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITISSLQDL 827

Query: 319 TLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMSLQSHLIPGLNLAAVGLFPA 378
TLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS SHLIPGLNLAAVGLFPA
Sbjct: 828 TLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS--SHLIPGLNLAAVGLFPA 1001

Query: 379 SSSAVPPPPSSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASAS 438
SSSAVPPPPSSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASAS
Sbjct: 1002SSSAVPPPPSSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASAS 1181

Query: 439 IKIAPPETPDSKVRMVITGPPEAQFKAQGRIYGLKEENFFGPKKEEVKLETHIRVPASA 498
IKIAPPETPDSKVRMV+ITGPPEAQFKAQGRIYGLKEENFFGPKKEEVKLETHIRVPASA

Sbjct: 1182IKIAPPETPDSDKVRMVIITGPPEAQFKAQGRIYGLKEENFFGPKEEVKLETHIRVPASA 1361

Query: 499 AGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRKIRDILA 558
AGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRKIRDILA

Sbjct: 1362AGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRKIRDILA 1541

Query: 559 QVKQQHQKGQSNLAQARRK 577

QVKQQHQKGQSN AQARRK

Sbjct: 1542QVKQQHQKGQSNQAQARRK 1598

CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 13,365

Number of Sequences: 0

Number of extensions: 8706

Number of successful extensions: 15

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 2

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

c-myc-CRD

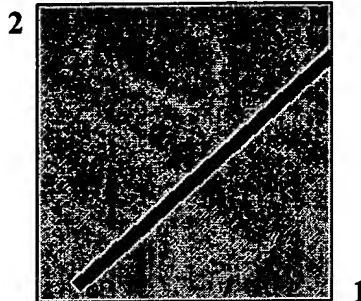
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:7

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** ☐ Filter ☐ Align

Sequence 1 lcl|seq_1 Length 577 (1 .. 577)

Sequence 2 lcl|seq_2 Length 1946 (1 .. 1946)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 963 bits (2489), Expect = 0.0
Identities = 493/499 (98%), Positives = 494/499 (98%)
Frame = +3

```
Query: 79  RSRKIQIRNIPPQLRWEVLDSLLAQYGTVENCEQVNTSESETAVVNVITYSNREQTRQAIMK 138
          RSRKIQIRNIPPQLRWEVLDSLLAQYGTVENCEQVNTSESETAVVNVITYSNREQTRQAIMK
Sbjct: 108 RSRKIQIRNIPPQLRWEVLDSLLAQYGTVENCEQVNTSESETAVVNVITYSNREQTRQAIMK 287

Query: 139 LNQHLENHALKVSYPDEQITQGPENRRGGFGSRGQPRQGSPPVAAGAPAKQQPVDIPL 198
          LNQHLENHALKVSYPDEQI QGPENRRGGFGSRGQPRQGSPPVAAGAPAKQQ VDIPL
Sbjct: 288 LNQHLENHALKVSYPDEQIAQGPENRRGGFGSRGQPRQGSPPVAAGAPAKQQQVDIPL 467

Query: 199 RLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEGCSACK 258
          RLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEGCSACK
Sbjct: 468 RLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEGCSACK 647

Query: 259 MILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLLIGKEGRNLKKVEQDTETKITISSLODL 318
          MILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLLIGKEGRNLKKVEQDTETKITISSLODL
Sbjct: 648 MILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLLIGKEGRNLKKVEQDTETKITISSLODL 827

Query: 319 TLYNPERTITVKGAIECCRAEQEIMKKVREAYENDVAAMSLQSHLIPGLNLAAVGLFPA 378
          TLYNPERTITVKGAIECCRAEQEIMKKVREAYENDVAAMS SHLIPGLNLAAVGLFPA
Sbjct: 828 TLYNPERTITVKGAIECCRAEQEIMKKVREAYENDVAAMS--SHLIPGLNLAAVGLFPA 1001

Query: 379 SSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKQHIKQLSRFASAS 438
          SSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKQHIKQLSRFASAS
Sbjct: 1002SSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKQHIKQLSRFASAS 1181

Query: 439 IKIAPPETPDSKVRMVVITGPPEAQFKAQGRIYGKLKEENFFGPKKEEVKLETHIRVPASA 498
          IKIAPPETPDSKVRMV+ITGPPEAQFKAQGRIYGKLKEENFFGPKKEEVKLETHIRVPASA
```

Sbjct: 1182IKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEENFFGPKKEEVKLETHIRVPASA 1361

Query: 499 AGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRKIRDILA 558
AGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRKIRDILA

Sbjct: 1362AGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRKIRDILA 1541

Query: 559 QVKQOHQKGQSNLAQARRK 577
QVKQOHQKGQSN AQARRK

Sbjct: 1542QVKQOHQKGQSNQAQARRK 1598

CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 13,365

Number of Sequences: 0

Number of extensions: 8706

Number of successful extensions: 15

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 2

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)



Blast 2 Sequences results

PubMed

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BLAST

OMIM

Taxonomy

Structure

c-myc-CRD

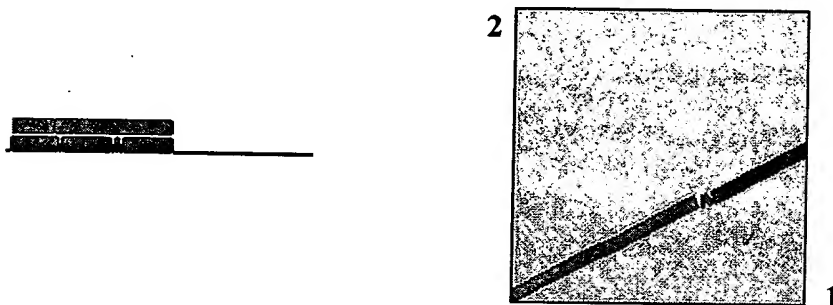
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:8

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align ☐

Sequence 1 lcl|seq_1 Length 577 (1 .. 577)

Sequence 2 lcl|seq_2 Length 3283 (1 .. 3283)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 742 bits (1916), Expect = 0.0

Identities = 381/579 (65%), Positives = 458/579 (78%), Gaps = 2/579 (0%)

Frame = +1

```
Query: 1  MNKLYIGNLNESVTPADLEKVFAEHKISYSGQFLVKSGYAFVDCPDEHWAMKAIETFS GK 60
          MNKLYIGNL+ +VT DL ++F + K+ +GQ L+KSGYAFVD PD++WA++AIET SGK
Sbjct: 73  MNKLYIGNLSPAVTADDLRQLFGDRKLPLAGQVLLKSGYAFVDYPDQNWAIETLSGK 252

Query: 61  VELQGKRLEMEHSVPKKQRSRKIQIRNIPPQLRWEVLDSLLAQYGTVENCEQVNTSEETA 120
          VEL GK +E+++SV KK RSRKIQIRNIPP L+WEVLD LLAQYGTVEN EQVNT++ETA
Sbjct: 253  VELHGKIMEVDYSVSKKLSRKIQIRNIPHLQWEVLDGLLAQYGTVENVEQVNTDTETA 432

Query: 121  VVNVTYSNREQTRQAIMKLNQHLENHALKVSYPDEQITQG--PENGRRGGFGSRGQPR 178
          VVNVTY+ RE+ + A+ KL+GHQ EN++ K+SYIPDE+++ P+ +RG SR Q
Sbjct: 433  VVNVTYATREEAKIAMEKLSGHQFENYSFKISYIPDEEVSSPSPQRAQRGDHSSREQGH 612

Query: 179  QGSPVAAGAPAKQQPVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAG 238
          A G ++ + +D PLR+LVPTQ+VGAIIGKEG TI+NITKQTQS++D+HRKEN+G
Sbjct: 613  -----APGGTSQARQIDFPLRLVPTQFVGAIIGKEGLTIKNITKQTQSRVDIHRKENS 777

Query: 239  AAEKAISVHSTPEGCSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLLIGKEGRN 298
          AAEK +++H+TPEG S AC+MILEIM KEA +TK A+E+PLKILAHN VGRLLIGKEGRN
Sbjct: 778  AAEKPVTIHATPEGTSEACRMILEIMQKEADETKLAEIPLKILAHNGLVGRLLIGKEGRN 957

Query: 299  LKKVEQDTETKITISSLQDLTLNPERTITVKGAIECCRAEQEIMKKVREAYENDVAAM 358
          LKK+E +T TKITISSLQDL++YNPERTITVKG +E C AE EIMKK+REA+END+ A+
Sbjct: 958  LKKIEHETGTKITISSLQDLISIYNPERTITVKGTVACASAEIEMKKLREAFENDMLAV 1137

Query: 359  SLQSHLIPGLNLAAGLFPASSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVG 418
          + S G F SS P P+ PEQE+V +FIP QAVG
```

Sbjct: 1138NTHS-----GYF---SSLYPHHQFG-----PFPHHSYPEQEIVNLFIPTQAVG 1260
Query: 419 AIIGKKGQHILSRFASASIKIAPPETPDSKVRMVITGPPEAQFKAQGRIYGKLKEEN 478
AIIGKKG HIKQL+RFA ASIKIAP E PD RMV+ITGPPEAQFKAQGRI+GKLKEEN
Sbjct: 1261AIIGKKGAHIKQLARFAGASIKIAPAEGPDVSERMVITGPPEAQFKAQGRIFGKLKEEN 1440
Query: 479 FFGPKKEEVKLETHIRVPASAAGRVIGKGGKTVNELQNLTAAEVVPRDQTPDENDQVIVK 538
FF PKEEVKLE HIRVP+S AGRVIGKGGKTVNELQNLT+AEV+VPRDQTPDEN++VIV+
Sbjct: 1441FFNPKEEVKLEAHIRVPSSTAGRVIGKGGKTVNELQNLTSAEVIVPRDQTPDENEEVIVR 1620
Query: 539 IIGHFYASQMAQRKIRDILAQVKQHQKQGSNLAQARRK 577
IIGHF+ASQ AQRKIR+I+ QVKQQ QK +A R K
Sbjct: 1621IIGHFFASQTAQRKIREIVQQVKQEQKYPQGVASQSRK 1737

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 20,909

Number of Sequences: 0

Number of extensions: 14230

Number of successful extensions: 17

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 3

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 3

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

MIM

Taxonomy

Structure

c-myc-CRD

BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:8

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align ☐

Sequence 1 lc|seq_1 Length 577 (1 .. 577)

Sequence 2 lc|seq_2 Length 3283 (1 .. 3283)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 742 bits (1916), Expect = 0.0

Identities = 381/579 (65%), Positives = 458/579 (78%), Gaps = 2/579 (0%)

Frame = +1

```

Query: 1  MNKLYIGNLNESVTPADLEKVF AEHKISYSGQFLVKSGYAFVDCPDEHWAMKAIETFS GK 60
          MNKLYIGNL+ +VT DL ++F + K+ +GQ L+KSGYAFVD PD++WA++AIET SGK
Sbjct: 73  MNKLYIGNLSPAVTADDLRQLFGDRKLPLAGQVLLKSGYAFVDYPDQNWAIETLS GK 252

Query: 61  VELQGRLEMEHSVPKKQSRKIQIRNIPPQLRWEVLDSL LAQYGTVENCEQVNTES ETA 120
          VEL GK +E+++SV KK RSRKIQIRNIPP L+WEVLD LLAQYGTVEN EQVNT++ETA
Sbjct: 253  VELHGKIMEVDYSVSKLRSRKIQIRNIPHLQWEVLDGLLAQYGTVENVEQVNTDT ETA 432

Query: 121  VVNVITYSNREQTRQAIMKLNGHQLENHALKVSYIPDEQITQG--PENGRRGGFGSRGQPR 178
          VVNVTY+ RE+ + A+ KL+GHQ EN++ K+SYIPDE+++ P+ +RG SR Q
Sbjct: 433  VVNVTYATREEAKIAMEKLSGHQFENYSFKISYIPDEEVSSPSPQRAQRGDHSSREQGH 612

Query: 179  QGSPVAAGAPAKQQPVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAG 238
          A G ++ + +D PLR+LVPTQ+VGAIIGKEG TI+NITKQTQS++D+HRKEN+G
Sbjct: 613  -----APGGTSQARQIDFPLRILVPTQFVGAIIGKEGLTIKNITKQTQSRVDIHRKENSG 777

Query: 239  AAEKAISVHSTPEGCSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLLIGKEGRN 298
          AAEK +++H+TPEG S AC+MILEIM KEA +TK A+E+PLKILAHN VGRLLIGKEGRN
Sbjct: 778  AAEKPVTIHATPEGTSEACRMILEIMQKEADETKLAEEIPLKILAHNGLVGRLLIGKEGRN 957

Query: 299  LKKVEQDTETKITISSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAM 358
          LKK+E +T TKITISSLQDL++YNPERTITVKG +E C AE EIMKK+REA+END+ A+
Sbjct: 958  LKKIEHETGKITISSLQDL SIYNPERTITVKGTVEACASAEIEIMKKLREAFENDMLAV 1137

Query: 359  SLQSHLIPGLNLAAVGLFPASSSAVPPPPSSVTGAAPYSSFMQAP EQEMVQVFIPAQAVG 418
          + S G F SS P P+ PEQE+V +FIP QAVG

```


Sbjct: 1138NTHS-----GYF---SSLYPHHQFG-----PFPHHSYPEQEIVNLFIPTQAVG 1260

Query: 419 AIIGKKGQHILSRFASASIKIAPPETPSKVRMVVITGPPEAQFKAQGRIYGKLKEEN 478
AIIGKKG HIKQL+RFA ASIKIAP E PD RMV+ITGPPEAQFKAQGRI+GKLKEEN

Sbjct: 1261AIIGKKGAHIKQLARFAGASIKIAPAEGPDVSERMVITGPPEAQFKAQGRIFGKLKEEN 1440

Query: 479 FFGPKKEEVKLETHIRVPASAAGRVIGKGGKTVNELQNLTAEEVVPRDQTPDENQVIVK 538
FF PKEEVKLE HIRVP+S AGRVIGKGGKTVNELQNLTAEV+VPRDQTPDEN++VIV+

Sbjct: 1441FFNPKEEVKLEAHIRVPSSTAGRVIGKGGKTVNELQNLTAEEVIVPRDQTPDENEEVIVR 1620

Query: 539 IIGHFYASQMAQRKIRDILAQVKQHQKQSNLAQARRK 577
IIGHF+ASQ AQRKIR+I+ QVKQQ QK +A R K

Sbjct: 1621IIGHFFASQTAQRKIREIVQQVKQEQKYPQGVASQRSK 1737

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 20,909

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length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)